

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 16:04:41 ; Search time 39 Seconds
(without alignments)

350.328 Million cell updates/sec

Title: US-10-723-083-2

Perfect score: 765

Sequence: 1 MHVHHHSSGIEGRMAPARS.....ENLKDLLVLPDCWEPVOE 142

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	673	88.0	144	1	FQHUGM
2	548	71.6	144	2	JH0469
3	544	71.1	144	1	A61632
4	480.5	62.8	143	1	FQBOGM
5	473	61.8	144	2	A44936
6	441	57.6	127	2	I46269
7	367.5	48.0	153	1	FQMSGM
8	84.5	11.0	2493	2	S72349
9	81	10.6	305	2	A56554
10	81	10.6	359	2	A55839
11	80.5	10.5	285	2	A42390
12	80.5	10.5	2493	2	S26372
13	79	10.3	610	2	A57632
14	78.5	10.3	329	2	T45972
15	78	10.2	496	2	S25091
16	78	10.2	816	2	S05548
17	78	10.2	1019	2	T00117
18	77.5	10.1	420	2	T39712
19	77.5	10.1	427	2	T42516
20	75.5	9.9	292	2	I51171
21	75.5	9.9	942	2	JC2129
22	75.5	9.9	1016	1	A46079
23	75	9.8	605	1	Q0B529
24	74.5	9.7	384	2	T41302
25	74.5	9.7	1305	2	T18548
26	73.5	9.6	248	2	T02647
27	73.5	9.6	1622	2	JE0378
28	73	9.5	234	2	T26429
29	73	9.5	461	2	S34472

30 73 9.5 943 2 T03306
31 73 9.5 1183 2 A89135
32 73 9.5 1496 2 T00499
33 72.5 9.5 289 2 D83709
34 72.5 9.5 417 2 C32185
35 72 9.4 311 2 G86383
36 72 9.4 447 2 A34582
37 72 9.4 770 2 P00105
38 71.5 9.3 530 2 D70476
39 71.5 9.3 1273 2 T00338
40 71 9.3 398 1 TVFVVR
41 71 9.3 611 2 F82951
42 70.5 9.2 265 2 T46089
43 70.5 9.2 601 1 B56564
44 70.5 9.2 633 1 A26030
45 70.5 9.2 1025 2 H81751

ALIGNMENTS

RESULT 1

FQHUGM

granulocyte-macrophage colony-stimulating factor precursor [validated] - human
N;Alternate names: colony-stimulating factor 2; GM-CSF

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004

C;Accession: C24636; I59065; A01853; A44175; JC1090

R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.

EMBL J. 4. 2561-2568, 1985

A;Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating

A;Reference number: A91015; MUID:86030234; PMID:3876930

A;Accession: C24636

A;Molecule type: DNA

A;Residues: 1-144 <MY>

A;Cross-references: UNIPROT:P04141; EMBL:X03021; NID:G31858; PIDN:CAA26822.1; PID:G31859

R;Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J.W.

Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986

A;Title: Genomic cloning, characterization, and multilineage growth-promoting activity of

A;Reference number: I59065; MUID:86205844; PMID:3486413

A;Accession: I59065

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-144 <RES>

A;Cross-references: GB:M13207; NID:G181147; PIDN:AAA98768.1; PID:G181148

R;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.

Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985

A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage colony-stim

A;Reference number: A25169; MUID:85298329; PMID:3898082

A;Accession: A25169

A;Molecule type: mRNA

A;Residues: 1-144 <CAN>

A;Cross-references: GB:M11734; NID:G181149; PIDN:AAAS2122.1; PID:G181150

R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Rennick, I

Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4364, 1985

A;Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor 1

A;Reference number: A01853; MUID:85242684; PMID:3925454

A;Accession: A01853

A;Molecule type: mRNA

A;Residues: 1-144 <LEE>

A;Cross-references: GB:M11220; NID:G183363; PIDN:AAAS2578.1; PID:G183364

R;Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary, A.C.; Luxenberg, D.P.; J

A.; Clark, S.C.

Science 228, 810-815, 1985

A;Title: Human GM-CSF: molecular cloning of the complementary DNA and purification of th

A;Reference number: A44175; MUID:85218749; PMID:3923623

A;Accession: A44175

A;Molecule type: mRNA

A;Residues: 1-116, 'T', 118-144 <WON>

A;Cross-references: GB:M10663; NID:G181145; PIDN:AAAS2121.1; PID:G181146

A;Note: parts of this sequence, including the amino end of the mature protein, were conf

R;Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.

Acta Biochim. Biophys. Sin. 25, 651-655, 1993

A:Title: Amplification of human granulocyte-macrophage colony-stimulating factor cDNA with
A:Reference number: JCI090
A:Accession: JCI090
A:Molecule type: protein
A:Residues: 18-21, 'C', 23-96, 'L', 98-144 <WEN>
C:Genetics:
A:Gene: GDB:CSF2
A:Cross-references: GDB:119812; OMIM:138960
A:Map position: 5q23.2-5q31.1
A:Introns: 53/3; 67/3; 109/3
C:Function:

A:Description: Stimulates the differentiation and proliferation of hematopoietic progenitor cells.
A:Superfamily: granulocyte-macrophage colony-stimulating factor
C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-144/Product: granulocyte-macrophage colony-stimulating factor #status experimental
F:44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.0%; Score 673; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPQWEHVNAIQEARLLNLSRDTAAENNETVEVISEMFDLQEPDCLQTRLE 75

DB 18 APARSPSPQWEHVNAIQEARLLNLSRDTAAENNETVEVISEMFDLQEPDCLQTRLE 77

QY 76 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 135

DB 78 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 137

QY 136 CWPVQOE 142

DB 138 CWPVQOE 144

RESULT 2

JH0469
granulocyte-macrophage colony-stimulating factor precursor - sheep
N:Alternate names: colony-stimulating factor 2; GM-CSF
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0469; S16730
R:McInnes, C.J.; Haig, D.M.
Gene 105, 275-279, 1991

A:Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-stimulating factor
A:Reference number: JH0469; MUID:92039044; PMID:1337025

A:Accession: JH0469
A:Molecule type: mRNA
A:Residues: 1-144 <MC1>
A:Cross-references: UNIPROT:P28773; GB:X53561; NID:g1800; PIDN:CAA37632.1; PID:g1801

C:Comment: This protein is a glycoprotein cytokine produced and secreted by various cell types.
C:Superfamily: granulocyte-macrophage colony-stimulating factor
C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-144/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA>
F:44/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.6%; Score 548; DB 2; Length 144;
Best Local Similarity 80.3%; Pred. No. 2.6e-45;
Matches 102; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 16 APARSPSPQWEHVNAIQEARLLNLSRDTAAENNETVEVISEMFDLQEPDCLQTRLE 75

DB 18 APTRQSPVTRPQWHDVAIKEALSLNLSRDTAAVMDTEVVSEMFDSQEPDCLQTRLE 77

QY 76 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 135

DB 78 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 137

QY 136 CWPVQOE 142

DB 138 CWPVQOE 144

RESULT 3

A61632

granulocyte-macrophage colony-stimulating factor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A61632
R:O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
Immunol. Cell Biol. 69, 51-55, 1991

A:Title: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stimulating factor
A:Reference number: A61632; MUID:91331592; PMID:1869289

A:Accession: A61632
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-144 <OAB>

A:Cross-references: UNIPROT:Q9MYK4; GB:X55991; NID:g6983759; PIDN:CAA39463.1; PID:g6983759
C:Superfamily: granulocyte-macrophage colony-stimulating factor
F:1-17/Domain: signal sequence #status predicted <SIG>

Query Match 71.1%; Score 544; DB 1; Length 144;
Best Local Similarity 79.5%; Pred. No. 6.4e-45;
Matches 101; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 16 APARSPSPQWEHVNAIQEARLLNLSRDTAAENNETVEVISEMFDLQEPDCLQTRLE 75

DB 18 APTRQSPVTRPQWHDVAIKEALSLNLSRDTAAVMDTEVVSEMFDSQEPDCLQTRLE 77

QY 76 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 135

DB 78 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 137

QY 136 CWPVQOE 142

DB 138 CWPVQOE 144

RESULT 4

FOBOGM

granulocyte-macrophage colony-stimulating factor precursor - bovine
N:Alternate names: colony-stimulating factor 2; GM-CSF
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: JI0037
R:Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall, J.M.; Picha, K.S.; Cosman
Mol. Immunol. 25, 843-850, 1988

A:Title: Bovine GM-CSF: molecular cloning and biological activity of the recombinant protein
A:Reference number: JI0037; MUID:89096971; PMID:3062386

A:Accession: JI0037
A:Molecule type: mRNA
A:Residues: 1-143 <MAL>

A:Cross-references: UNIPROT:P11052
C:Comment: This glycoprotein induces granulocyte, macrophage, and eosinophil colony formation.
C:Superfamily: granulocyte-macrophage colony-stimulating factor
C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-143/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA>
F:44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.8%; Score 480.5; DB 1; Length 143;
Best Local Similarity 68.5%; Pred. No. 7.6e-39;
Matches 87; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

QY 16 APARSPSPQWEHVNAIQEARLLNLSRDTAAENNETVEVISEMFDLQEPDCLQTRLE 75

DB 18 APTRPENTATRPQWHDVAIKEALSLNLSRDTAAVMDT-EVVSEKFDQEPDCLQTRLK 76

QY 76 LYKQGLRGSITKLKGLPTWASHYKHCPTPTSCATQIITFESKFNKDLFLVIPPED 135

DB 77 LYKNGLGSLTSLMGSLTWASHYKHCPTPTSCGTQIFGKFNKDLKEFLFIIPED 136

QY 136 CWPVQOE 142

DB 137 CWPVQOE 143

RESULT 5

A44936
granulocyte-macrophage colony-stimulating factor precursor - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: A44936
R;Nash, R.A.; Schuening, F.; Appelbaum, F.; Hammond, W.P.; Boone, T.; Morris, C.F.; Slick
Blood 78, 930-937, 1991
A/Title: Molecular cloning and in vivo evaluation of canine granulocyte-macrophage colony
A/Reference number: A44936; MUID:91329842; PMID:1868252
A/Accession: A44936
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-144 <NAS>
A/Cross-references: UNIPROT:P48749; GB:S49738; PIDN:AAAB19466.1; PID:G233567
A/Note: sequence extracted from NCBI backbone (NCBIN:49738, NCBI:P:49739)
C/Superfamily: granulocyte-macrophage colony-stimulating factor
F:1-17/Domain: signal sequence #status predicted <SIG>

Query Match 61.8%; Score 473; DB 2; Length 144;
Best Local Similarity 68.5%; Pred. No. 4e-38;
Matches 87; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

QY 16 APARSPSPQPEHVNIAQEARLLNLSRDTAAENNETVEVISEMFDLOEPTCLOTRL 75

DB 18 APRSPPTLVTRPSQHVDAIQEALSLLNNSNDVTAVNKAQVSEVDFPGEPTCLETRLQ 77

QY 76 LYKQGLRGSUTLKGPLTMASHYKQHCPTPTSCATOLIITPESKFNKDLFLVIPP 135

DB 78 LYKEGLOGSUTSLKNPLTMANHYKQHCPTPTSPCATINPKSFKNKDLFLNIPP 137

QY 136 CWEPVOE 142

DB 138 CWKPVK 144

RESULT 6

I46269
granulocyte-macrophage colony stimulating factor - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C/Accession: I46269
R;Smith, L.R.; Lundeen, K.A.; Diveley, J.P.; Carlo, D.J.; Brostoff, S.W.
Immunogenetics 39, 80, 1994
A/Title: Nucleotide sequence of the Lewis rat granulocyte-macrophage colony stimulating
A/Reference number: I46269; MUID:94041474; PMID:8225444
A/Accession: I46269
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-127 <SMI>
A/Cross-references: UNIPROT:P48750; EMBL:U00620; NID:G392779; PIDN:AAAL8281.1; PID:G3927
C/Superfamily: granulocyte-macrophage colony-stimulating factor

Query Match 57.6%; Score 441; DB 2; Length 127;
Best Local Similarity 63.0%; Pred. No. 4e-35;
Matches 80; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 16 APARSPSPQPEHVNIAQEARLLNLSRDTAAENNETVEVISEMFDLOEPTCLOTRL 75

DB 1 APRSPNPVTRPWKHVDIAKEALSLLNDMPALENKNEDVDIISNFSIQRTCVQTRLK 60

QY 76 LYKQGLRGSUTLKGPLTMASHYKQHCPTPTSCATOLIITPESKFNKDLFLVIPP 135

DB 61 LYKQGLRGNLTUNGALTMASHYQVNCPTPTPTDCEIETVTFEDFKNLKGLFLDIPP 120

QY 136 CWEPVOE 142

DB 121 CWKPVK 127

RESULT 7

Query Match 48.0%; Score 367.5; DB 1; Length 153;
Best Local Similarity 54.3%; Pred. No. 5.5e-28;
Matches 69; Conservative 23; Mismatches 32; Indels 3; Gaps 1;

FQMSGM

granulocyte-macrophage colony-stimulating factor precursor - mouse
N/Alternate names: colony-stimulating factor 2; GM-CSF; integral membrane protein
C/Species: Mus musculus (house mouse)
C/Date: 28-Aug-1985 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: I48368; I48369; A24636; A24645; A24644; A01854; A21882
R;Gough, N.M.; Metcalf, D.; Gough, J.; Grail, D.; Dunn, A.R.
EMBO J. 4, 645-653, 1985
A/Title: Structure and expression of the mRNA for murine granulocyte-macrophage colony st
A/Reference number: I48368; MUID:85230531; PMID:3874057
A/Accession: I48368
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-153 <RES>
A/Cross-references: UNIPROT:P01587; EMBL:X02333; NID:G51103; PIDN:CAA26192.1; PID:G51104
A/Accession: I48369
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 13-153 <RE2>
A/Cross-references: EMBL:X02333; NID:G51103; PIDN:CAA26193.1; PID:G51106
R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
EMBO J. 4, 2561-2568, 1985
A/Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating
A/Reference number: A91015; MUID:86030234; PMID:3876930
A/Accession: A24636
A/Molecule type: DNA; mRNA
A/Residues: 13-150, 'G', 152-153 <MIY>
A/Residues: 13-150, 'G', 152-153 <MIY>
A/Cross-references: GB:X03020; NID:G51098; PIDN:CAA26821.1; PID:G51099
A/Note: the sequence translated from the mRNA differs from that of the DNA in having 151-
R;Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn, A.R.
EMBO J. 4, 2569-2573, 1985
A/Title: The structure and expression of the murine gene encoding granulocyte-macrophage
A/Reference number: A24645; MUID:86030235; PMID:3876931
A/Accession: A24645
A/Molecule type: DNA
A/Residues: 13-150, 'G', 152-153 <STA>
A/Cross-references: GB:X03020; NID:G51098; PIDN:CAA26821.1; PID:G51099
R;DeLamarter, J.F.; Mermoud, J.J.; Liang, C.M.; Eliason, J.F.; Thatcher, D.R.
EMBO J. 4, 2575-2581, 1985
A/Reference number: A24644; MUID:86030236; PMID:3902470
A/Accession: A24644
A/Molecule type: mRNA
A/Residues: 13-153 <DE>
A/Cross-references: GB:X03019; NID:G51100; PIDN:CAA26820.1; PID:G736260
R;Gough, N.M.; Gough, J.; Metcalf, D.; Kelso, A.; Grail, D.; Nicola, N.A.; Burgess, A.W.
Nature 309, 763-767, 1984
A/Title: Molecular cloning of cDNA encoding a murine haematopoietic growth regulator, gra
A/Reference number: A01854; MUID:84245825; PMID:6610831
A/Accession: A01854
A/Molecule type: mRNA
A/Residues: 36, 'I', 38-150, 'S', 152-153 <GOU>
A/Cross-references: GB:X05906; NID:G51096; PIDN:CAA29336.1; PID:G51097
A/Experimental source: lung tissue
R;Sparrow, L.G.; Metcalf, D.; Hunkapiller, M.W.; Hood, L.E.; Burgess, A.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 292-296, 1985
A/Title: Purification and partial amino acid sequence of asialo murine granulocyte-macro
A/Reference number: A21882; MUID:85113187; PMID:3871523
A/Accession: A21882
A/Molecule type: protein
A/Residues: 36, 'I', 38-59 <SPA>
C/Comment: It is unclear if Met-1 or Met-13 is the initiator.
C/Genetics:
A/Introns: 62/3; 76/3; 118/3
C/Superfamily: granulocyte-macrophage colony-stimulating factor
C/Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-153/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F:95,104/Binding site: carboxydrate (Asn) (covalent) #status predicted

QY 16 APARSPSPTOPWEHVNAIQEARLLNLSDTYAAENNETVEVISEMFDLQETCLQTRLE 75
DB 30 APTRSPTITVRPKHVEAIKEA---LNLDDMEVITNEEVVSVNFSFKKUTCVCQTRUK 86
QY 76 LYKQGLRGLSLTKLKGPLTMASHYKHQCPPTPETS CATQIITTFESPKENLKDFLLVIPED 135
DB 87 IFQGLRGNTFKLKGALNMTASYQIYCYPTPETDCTQVTVYADFIDSILKPLTDIPE 146
QY 136 CWEPVQE 142
DB 147 CKKPVQK 153
RESULT 8
S72349
nonstructural polyprotein - eastern equine encephalomyelitis virus
N;Alternate names: nonstructural protein NSP1; nonstructural protein NSP2; nonstructural
C;Species: eastern equine encephalomyelitis virus
C;Date: 04-May-1998 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
C;Accession: S72349
R;Weaver, S.C.; Hagenbaugh, A.; Ballew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.J.
Virology 197, 375-390, 1993
A;Title: A comparison of the nucleotide sequences of eastern and western equine encephal
A;Reference number: S72349; MUID:94025587; PMID:8105605
A;Accession: S72349
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-2493 <WEA>
A;Cross-references: UNIPROT:Q88789; EMBL:U01034; NID:g9393006; PIDN:AAEC53734.1; PID:g939300
A;Note: readthrough of the terminator UGA occurs between the codons AAU for residue 1878
A;Note: the readthrough stopcodon UGA for residue 1879 is translated as X
C;Superfamily: Semliki Forest virus nonstructural protein
Query Match 11.0%; Score 84.5; DB 2; Length 2493;
Best Local Similarity 26.1%; Pred. No. 21;
Matches 36; Conservative 17; Mismatches 54; Indels 31; Gaps 7;
QY 17 PARSPSPSTOPWEHVNAIQEARLLNLSDTYAAENNETVEV----- 57
DB 1678 PARIPSP---PCTSTNG--STTSIQSLGSDQSASAGSAGSIVDHSVLSIPSATGPDVR 1732
QY 58 ISEMFIDQET--CLQTRLELY-KQGLRGLSLTKLKGPLTMASHYKHQC-PPTPETS--- 110
DB 1733 TSSLSLSEQPTFTPMVVEAEIHASQWSLSPISITGSETRVPPSPQDSRPSTPSGSH 1792
QY 111 CATQIITTFESPKENLKDF 128
DB 1793 TSVDLITFDSVAETLEDF 1810
RESULT 9
A56554
transcription factor C/EBP - African clawed frog
N;Alternate names: CCAAT/enhancer core binding protein
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56554
R;Xu, Q.; Tata, J.R.
Mach. Dev. 38, 69-81, 1992
A;Title: Characterization and developmental expression of Xenopus C/EBP gene.
A;Reference number: A56554; MUID:92399265; PMID:1525039
A;Accession: A56554
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <XUL>
A;Cross-references: UNIPROT:Q91346; GB:S44193; NID:g255566; PIDN:AAE23276.1; PID:g255566
A;Note: sequence extracted from NCBI backbone (NCBI:113707, NCBI:113708)
C;Superfamily: CCAAT/enhancer-binding protein alpha
C;Keywords: DNA binding; leucine zipper; transcription factor
Query Match 10.6%; Score 81; DB 2; Length 305;
Best Local Similarity 29.3%; Pred. No. 3.6;
Matches 34; Conservative 17; Mismatches 35; Indels 30; Gaps 7;

Db 142 PAKQQRREHLEALQTESRTL-IFYBSPHRLRLTQDLAEVGSWDQRQIVLARELTKLYEE 200
QY 80 GLRGSUTLKGPLTMMASHYKQHC-----PTPETS CATQIITFESPKENLKDF 128
Db 201 FWRSGICE-----ALAHYQKEPQGEYTLVAGNPPSET-----LLTTEQLKAEQLQL 248
QY 129 LL 130
Db 249 MM 250

RESULT 12
S26372
nonstructural polyprotein - eastern equine encephalomyelitis virus
N;Contains: nonstructural protein NSP1; nonstructural protein NSP2; nonstructural protein
C;Species: eastern equine encephalomyelitis virus
C;Date: 06-Jan-1994 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
A;Accession: S26369; S26372
R;Volchkov, V.E.; Volchikova, V.A.; Netesov, S.V.
Mol. Gen. Microbiol. Virusol. 5, 8-15, 1991
A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus gene
A;Reference number: S26369; MUID:91375524; PMID:1896061
A;Accession: S26369
A;Molecule type: genomic RNA
A;Residues: 1-2493 <VOL>
A;Cross-references: UNIPROT:Q66581; EMBL:X63135
A;Note: sequence could not be checked because of bad print in paper
A;Note: readthrough of the terminator UGA occurs between the codons AAU for residue 1878
A;Note: the readthrough stopcodon UGA for residue 1879 is translated as X
A;Accession: S26372
A;Molecule type: mRNA
A;Residues: 1886-2493 <VO2>
A;Cross-references: EMBL:X63135; NID:959185; PIDN:CAA44847.1; PID:g1334981
A;Note: sequence could not be checked because of bad print in paper
A;Note: this reading frame extends between two stop codons and does not begin with a sta
C;Superfamily: Semliki Forest virus nonstructural protein
C;Keywords: nonstructural protein; polyprotein
F;1-532/Product: nonstructural protein NSP1 #status predicted <NS1>
F;533-1326/Product: nonstructural protein NSP2 #status predicted <NS2>
F;1327-1878/Product: nonstructural protein NSP3 #status predicted <NS3>
F;1886-2493/Product: nonstructural protein NSP4 #status predicted <NS4>

Query Match 10.5%; Score 80.5; DB 2; Length 2493;
Best Local Similarity 27.8%; Pred. No. 52;
Matches 37; Conservative 19; Mismatches 56; Indels 21; Gaps 7;
QY 17 PARSPS-PSTQPEHVNAIQEARRLLNLSRDTAAEMN-ETVEV-----ISEMF 62
Db 1678 PARIPFPCTSTNGSTTSIQSLGEYQSASASSGAREISVDQVSLWSIPSATGFDVRTSSSL 1737
QY 63 DLOEPT--CLQTRLELY-KQGLRGSTLTKGPLTMMASHYKQHC-PPTPETS CA---TQI 115
Db 1738 SLEQPTFTPTMVVEAIIHASQGLWSIPSTIGETRVFSPSPQDSRPTSPASASHTFVDL 1797
QY 116 ITPESPKENLKDF 128
Db 1798 ITPDSVAIELEDF 1810

RESULT 13
A57632
homeotic protein BE1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
A;Accession: A57632
R;Reiser, L.; Modrusan, Z.; Margossian, L.; Samach, A.; Ohad, N.; Haughn, G.W.; Fischer,
Cell 83, 735-742, 1995
A;Title: The BE1 gene encodes a homeodomain protein involved in pattern formation in b
A;Reference number: A57632; MUID:96097117; PMID:8521490
A;Accession: A57632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-610 <REI>

A;Cross-references: UNIPROT:Q38897; GB:U39944; NID:g1122532; PIDN:AAB05099.1; PID:g1122532;
C;Genetics:
A;Gene: BE1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;391-450/Domain: homeobox homology <HOX>

Query Match 10.3%; Score 79; DB 2; Length 610;
Best Local Similarity 22.7%; Pred. No. 13;
Matches 27; Conservative 20; Mismatches 42; Indels 30; Gaps 4;
QY 2 HHHHHSSGIEGRMAPRSPSPSTQPEHVNAIQEARRLLNLSRDTAAEMNE-----TV 55
Db 72 HHHHHHQT-----SGTDQNQLLESSSAWRLCNVNDPFPSEVNDRRPQRP 119
QY 56 EIVSEMFDLQETCL-----QTRLELYKQGLRG-----SLTKLKGPLTMMASHYKQH 102
Db 120 QGLSLSLSSNPSTISLSQSFELRPQQQGGYSGKNGSTQHNLTQHTQMMMMNHHQNN 178

RESULT 14
T45972
hypothetical protein F9D24.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
A;Accession: T45972
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23011
A;Accession: T45972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <DAN>
A;Cross-references: UNIPROT:Q9M2K4; EMBL:AL137081
A;Experimental source: cultivar Columbia; BAC clone F9D24
C;Genetics:
A;Map position: 3
A;Introns: 208/2; 238/3; 281/1
A;Note: F9D24.30

Query Match 10.3%; Score 78.5; DB 2; Length 329;
Best Local Similarity 28.0%; Pred. No. 6.8;
Matches 21; Conservative 12; Mismatches 23; Indels 19; Gaps 3;
QY 2 HHHHHSSGIEGRMAPRSPSPSTQPEHVNAIQE-----ARRLLNLSR 45
Db 106 NHHHHHS--INGNVGPTRSSSTSTSPSDH-NSLSDDDDNNKEAPPSDHDHMDNNDNVANQNN 162
QY 46 DTAEMNVEIVEISE 60
Db 163 AAGNNYNESDEVQSQ 177

RESULT 15
S25091
cruciferin BnC2 - rape
C;Species: Brassica napus (rape)
C;Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
A;Accession: S25091
R;Breen, J.P.; Crouch, M.L.
Plant Mol. Biol. 19, 1049-1055, 1992
A;Title: Molecular analysis of a cruciferin storage protein gene family of Brassica napu
A;Reference number: S25090; MUID:92379259; PMID:1511129
A;Accession: S25091
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-496 <BRE>
A;Cross-references: UNIPROT:P33524; EMBL:X59295; NID:g17791; PIDN:CAA41985.1; PID:g7629292
C;Genetics:
A;Gene: BnC2
A;Introns: 95/1; 222/2; 362/3
C;Superfamily: glycinin
C;Keywords: seed; storage protein

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OM protein - protein search, using sw model

Run on: March 8, 2005, 15:56:25 ; Search time 177 Seconds
(without alignments)
410.821 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHSHSGIEGRMAPARS.....ENLKDFLLVLPDCEWPEVQE 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	673	88.0	144	1	CSF2_HUMAN
2	664	86.8	144	2	Q647J8
3	653	85.4	144	2	Q9GL44
4	633	82.7	144	2	Q865Y5
5	548	71.6	144	1	CSF2_SHEEP
6	544	71.1	144	2	Q9MYK4
7	528	69.0	144	1	CSF2_CEREL
8	527	68.9	146	2	Q8WN17
9	513	67.1	152	2	Q95L10
10	487	63.7	144	1	CSF2_PIG
11	486.5	63.6	143	2	Q6Q8A7
12	480.5	62.8	143	1	CSF2_BOVIN
13	473	61.8	144	1	CSF2_CANFA
14	472	61.7	141	2	Q7YRF7
15	451	59.0	144	1	CSF2_FELCA
16	451	57.6	127	1	CSF2_RAT
17	435.5	56.9	140	1	CSF2_CAVPO
18	422.5	55.2	141	2	Q8VH40
19	381.5	49.9	145	2	Q8CFB5
20	361	47.2	138	2	Q99J91
21	360.5	47.1	141	1	CSF2_MOUSE
22	209.5	27.4	90	2	Q80XG1
23	87	11.4	233	2	Q6ENY6
24	87	11.4	499	2	Q81YK2
25	85	11.1	354	2	Q8NDL5
26	85	11.1	499	2	Q8N7T5
27	84.5	11.0	196	1	HUNB_DROAA
28	84.5	11.0	2493	2	Q88789
29	83	10.8	424	2	Q647M8
30	83	10.8	785	2	Q8MQP8
31	83	10.8	909	2	Q8THK7

32	82.5	10.8	610	2	Q9CS72	Q9cs72 mus musculus
33	81.5	10.7	344	2	Q8RYL3	Q8ryl3 oryza sativ
34	81.5	10.7	965	2	Q8JZS5	Q8jzs5 rattus norv
35	81.5	10.7	1212	2	Q8K4T4	Q8k4t4 rattus norv
36	81	10.6	171	1	HUNB_SCAAL	O46254 scaptomyza
37	81	10.6	305	2	Q91346	Q91346 xenopus lae
38	81	10.6	343	2	Q9DG50	Q9dg50 xenopus lae
39	81	10.6	359	1	IKBB_MOUSE	Q60778 mus musculus
40	81	10.6	359	2	Q8VC27	Q8vc27 mus musculus
41	81	10.6	379	2	Q8SB73	Q8sb73 oryza sativ
42	81	10.6	379	2	Q7G6D7	Q7g6d7 oryza sativ
43	81	10.6	424	2	Q64E31	Q64e31 uncultured
44	80.5	10.5	285	2	Q8YN88	Q8yn88 anabaena sp
45	80.5	10.5	1371	2	Q7QRM3	Q7qrm3 giardia lam

ALIGNMENTS

RESULT 1
CSF2_HUMAN STANDARD; PRT; 144 AA.
ID _CSF2_HUMAN
AC P04141; Q8NFI6;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE (Colony-stimulating factor) (CSF) (Sargramostim) (Molgramostin).
GN Name-CSF2; Synonyms-GMCSF;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85242684; PubMed=3925454;
RA Lee F., Yokota T., Otsuka T., Gemmell L., Larson N., Luh J.,
RA Arai K.-I., Rennick D.;
RT "Isolation of cDNA for a human granulocyte-macrophage colony-
RT stimulating factor by functional expression in mammalian cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4360-4364(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205844; PubMed=3486413;
RA Kaushansky K., O'Hara P.J., Berkner K., Segal G.M., Hagen F.S.,
RA Adamson J.W.;
RT "Genomic cloning, characterization, and multilineage growth-promoting
RT activity of human granulocyte-macrophage colony-stimulating factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3101-3105(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85298329; PubMed=3898082;
RA Cantrell M.A., Anderson D., Cerretti D.P., Price V., McKereghan K.,
RA Tushinski R.J., Mochizuki D.Y., Larsen A., Grabstein K., Cosman D.;
RT "Cloning, sequence, and expression of a human granulocyte/macrophage
RT colony-stimulating factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6250-6254(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85218749; PubMed=3923623;
RA Wong G.G., Wittek J.S., Temple P.A., Wilkens K.M., Leary A.C.,
RA Luxenberg D.P., Jones S.S., Brown E.L., Kay R.M., Orr E.C.,
RA Shoenaker C., Golde D.W., Kaufman R.J., Hewick R.M., Wang E.A.,
RA Clark S.C.;
RT "Human GM-CSF: molecular cloning of the complementary DNA and
RT purification of the natural and recombinant proteins.";
RL Science 228:810-815(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=86030234; PubMed=3876930;
RA Miyatake S., Otsuka T., Yokota T., Lee F., Arai K.-I.;
RT "Structure of the chromosomal gene for granulocyte-macrophage colony
RT stimulating factor: comparison of the mouse and human genes.";

RL EMBO J. 4:2561-2568(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Kimmerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,
 RA Davis C.A., Kadner K., Miguel T., Pitluck S., Pollard M., Rojeski H.,
 RA Subramanian S., Martin C.H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A., AND VARIANTS ILE-115 AND THR-117.
 RA Riederer M.J., Carrington D.P., Chung M.-W., Lee C.L., Yi Q.,
 RA Nickerson D.A.;
 RL "SeattleSNPs: NHLBI HL6682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 18-144 FROM N.A., AND VARIANT THR-117.
 RC TISSUE=Peripheral blood;
 RA Bhattacharya P., Pandey G., Mukherjee K.J.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=92144609; PubMed=1737041;
 RA Kaushansky K., Lopez J.A., Brown C.B.;
 RT "Role of carbohydrate modification in the production and secretion of
 RT human granulocyte macrophage colony-stimulating factor in genetically
 RT engineered and normal mesenchymal cells.";
 RL Biochemistry 31:1881-1886(1992).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=92108420; PubMed=1837174;
 RA Diederichs K., Boone T., Karplus P.A.;
 RT "Novel fold and putative receptor binding site of granulocyte-
 RT macrophage colony-stimulating factor.";
 RL Science 254:1779-1782(1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=92235844; PubMed=1569568;
 RA Walter M.R., Cook W.J., Ealick S.E., Nagabhushan T.L., Trotta P.P.,
 RA Bugg C.E.;
 RT "Three-dimensional structure of recombinant human granulocyte-
 RT macrophage colony-stimulating factor.";
 RL J. Mol. Biol. 224:1075-1085(1992).
 CC -I- FUNCTION: Cytokine that stimulates the growth and differentiation
 CC of hematopoietic precursor cells from various lineages, including
 CC granulocytes, macrophages, eosinophils and erythrocytes.
 CC -I- SUBUNIT: Monomer.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- POLYMORPHISM: Variant Ile-117 may be a risk factor for atopic
 CC asthma.
 CC -I- PHARMACUTICAL: Available under the names Leukine (Immunex) and
 CC Leucomax (Novartis). Used in myeloid reconstitution following bone
 CC marrow transplant, bone marrow transplant engraftment failure or
 CC delay, mobilization and following transplantation of autologous
 CC peripheral blood progenitor cells, and following induction
 CC chemotherapy in older adults with acute myelogenous leukemia.
 CC -I- SIMILARITY: Belongs to the GM-CSF family.
 CC -I- DATABASE: NAME=Leukine; NOTE=Clinical information on Leukine;
 CC WWW="http://www.leukine.com/".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; M13207; AAA98768.1; -;
 DR EMBL; M11734; AAA52122.1; -;
 DR EMBL; M11220; AAA52578.1; -;
 DR EMBL; X03021; CAA26822.1; -;
 DR EMBL; M10663; AAA52121.1; -;
 DR EMBL; AC004511; AAC08707.1; -;.

DR EMBL; AF373868; AAK51563.1; -;
 DR EMBL; AF510855; AAM44054.1; -;
 DR PIR; C24636; FOHUGM.
 DR PDB; 1CSG; X-ray; A/B=18-144.
 DR PDB; 2GMF; X-ray; A/B=-.
 DR Genew; HGNC:2434; CSF2.
 DR MIM; 138960; -;
 DR GO; GO:0005129; F:granulocyte macrophage colony-stimulating f...; TAS.
 DR InterPro; IPR009079; 4.helix_cytokine.
 DR InterPro; IPR000773; GM_CSF.
 DR Pfam; PF01109; GM_CSF; 1.
 DR PRINTS; PR00693; GMCSFACTOR.
 DR ProDom; PD007349; GM_CSF; 1.
 DR SMART; SM00040; CSF2; 1.
 DR PROSITE; PS00702; GM_CSF; 1.
 KW 3D-structure; Cytokine; Growth factor; Pharmaceutical;
 KW Polymorphism; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 144
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT CARBOHYD 22 22
 FT CARBOHYD 24 24
 FT CARBOHYD 26 26
 FT CARBOHYD 27 27
 FT CARBOHYD 44 44
 FT CARBOHYD 54 54
 FT VARIANT 115 115
 FT VARIANT 117 117
 FT CONFLICT 96 96
 FT CONFLICT 123 123
 FT TURN 25 27
 FT HELIX 30 45
 FT HELIX 50 53
 FT TURN 54 54
 FT STRAND 56 60
 FT TURN 66 67
 FT HELIX 72 81
 FT TURN 82 82
 FT HELIX 85 90
 FT HELIX 91 104
 FT STRAND 115 119
 FT HELIX 120 131
 FT TURN 132 133
 SQ SEQUENCE 144 AA; 16295 MW; 75D1E50506BCA7A8 CRC64;
 Query Match 88.0%; Score 673; DB 1; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.4e-54;
 Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 APARSPSPQPEWHVNAIQEARRLLNLSRDAAENNETVEVISEMFDLOEPTCLQTRLE 75
 Db 18 APARSPSPQPEWHVNAIQEARRLLNLSRDAAENNETVEVISEMFDLOEPTCLQTRLE 77
 QY 76 LYKQGLRGSLLTKLKGPLTNWASHYKHCPTTSCATQIITFESEKLNKDFLLVLPD 135
 Db 78 LYKQGLRGSLLTKLKGPLTNWASHYKHCPTTSCATQIITFESEKLNKDFLLVLPD 137
 QY 136 CWEPVQE 142
 Db 138 CWEPVQE 144
 RESULT 2
 Q647J8 PRELIMINARY; PRT; 144 AA.
 ID Q647J8
 AC Q647J8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

```

DE Granulocyte-macrophage colony stimulating factor 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li C.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY720441; AAU21240.1; -.
SQ SEQUENCE 144 AA; 16269 MW; 75D1E0B9D4D1A1A8 CRC64;

Query Match 86.8%; Score 664; DB 2; Length 144;
Best Local Similarity 98.4%; Pred. No. 9.8e-54;
Matches 125; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 16 APARSPSPQTPWEHVNAIQEARRLLNSRDTAENNETVEVISEMFDLQEPCLQTRLE 75
DB 18 APCRSPSPQTPWEHVNAIQEARRLLNSRDTAENNETVEVISEMFDLQEPCLQTRLE 77
QY 76 LYKQGLRGLSTLTKGPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPP 135
DB 78 LYKQGLRGLSTLTKGPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPP 137
QY 136 CWEPVOE 142
DB 138 CWEPVOE 144

RESULT 4
ID Q865Y5 PRELIMINARY; PRT; 144 AA.
AC Q865Y5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor precursor.
GN Names=GM-CSF;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY234216; AAO85329.1; -.
DR HSSP; P04141; 2GMF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR PRINTS; PR00693; GMCSPFACTOR.
DR ProDom; PD007349; GM_CSF; 1.
DR SMART; SM00040; CSF2; 1.
DR PROSITE; PS00702; GM_CSF; 1.
KW Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 144 granulocyte-macrophage colony-stimulating factor precursor.
FT SEQUENCE 144 AA; 16220 MW; 2321CAE533040D04 CRC64;

Query Match 82.7%; Score 633; DB 2; Length 144;
Best Local Similarity 92.1%; Pred. No. 7.4e-51;
Matches 117; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 16 APARSPSPQTPWEHVNAIQEARRLLNSRDTAENNETVEVISEMFDLQEPCLQTRLE 75
DB 18 APARLSPGQTPWEHVNAIQEARRLLNSRDTAENNETVEVISEMFDLQEPSCVQTRLE 77
QY 76 LYKQGLRGLSTLTKGPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPP 135
DB 78 LYKQGLRGLSTLTKGPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPP 137
QY 136 CWEPVOE 142
DB 138 CWEPVOE 144

RESULT 5
ID CSF2 SHEEP STANDARD; PRT; 144 AA.
AC P2873;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE (Colony-stimulating factor) (CSF).
GN Names=CSF2;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92039044; PubMed=1937025; DOI=10.1016/0378-1119(91)90163-6;
 RA McInnes C.J., Haig M.C.K.;
 RT "Cloning and expression of a cDNA encoding ovine granulocyte-
 macrophage colony-stimulating factor.";
 RL Gene 105:275-279(1991).
 CC -1- FUNCTION: Cytokine that stimulates the growth and differentiation
 of hematopoietic precursor cells from various lineages, including
 granulocytes, macrophages, eosinophils and erythrocytes (By
 similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the GM-CSF family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X53561; CAA37632.1; ..
 DR PIR; JH0469; JH0469.
 DR HSSP; P04141; 2GMF.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR Pfam; PF01109; GM_CSF; 1.
 DR PRINTS; PR00693; GMCSPFACTOR.
 DR ProDom; PD007349; GM_CSF; 1.
 DR SMART; SM00040; CSF2; 1.
 DR PROSITE; PS00702; GM_CSF; 1.
 DR SIGNAL 1 17
 FT CYTOKINE; Glycoprotein; Growth factor; Signal.
 FT By similarity.
 FT CHAIN 18 144
 FT Granulocyte-macrophage colony-stimulating
 FT factor.
 FT DISULFID 71 113
 FT By similarity.
 FT DISULFID 105 138
 FT By similarity.
 FT CARBOHYD 44 44
 FT N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 144 AA; 16318 MW; ABAAC8733B580008 CRC64;
 Query Match 71.6%; Score 548; DB 1; Length 144;
 Best Local Similarity 80.3%; Pred. No. 5.7e-43;
 Matches 102; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 16 APARSPSPQWHEVNAIQEARRLLNLSRDTAAENNEIVEISEMFDLQEPICLQTRLE 75
 DB 18 APTROPSPVTRPQHWDAIKEALSLNDSITDAVMDTEVVEVSEMFDSQEPICLQTRLE 77
 QY 76 LYKQGLRGLSTLTKGLPLTMASHYKHCPPTPTSCATQIITPESPKENLKDFLLVIFPD 135
 DB 78 LYKQGLRGLSTLTKGLPLTMASHYKHCPPTPTSCATQIITPESPKENLKDFLLVIFPD 137
 QY 136 CWEPVQK 142
 DB 138 CWEPVQK 144
 RESULT 6
 QY Q9MYK4 PRELIMINARY; PRT; 144 AA.
 AC Q9MYK4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Granulocyte-macrophage colony-stimulating factor (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91331592; PubMed=1869289;
 RA O'Brien P.M., Rothel J.S., Seow H.F., Wood P.R.;
 RT "Cloning and sequencing of the cDNA for ovine granulocyte-Macrophage
 colony stimulating factor (GM-CSF).";
 RL Immunol. Cell Biol. 69:51-55(1991).
 CC -1- FUNCTION: Cytokine that stimulates the growth and differentiation
 of hematopoietic precursor cells from various lineages, including
 granulocytes, macrophages, eosinophils and erythrocytes (By
 similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X55991; CAA39463.1; ..
 DR PIR; A61632; A61632.
 DR HSSP; P04141; 2GMF.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005129; F:granulocyte macrophage colony-stimulating f...; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR Pfam; PF01109; GM_CSF; 1.
 DR PRINTS; PR00693; GMCSPFACTOR.
 DR ProDom; PD007349; GM_CSF; 1.
 DR SMART; SM00040; CSF2; 1.
 DR PROSITE; PS00702; GM_CSF; 1.
 DR CHAIN 1 >144
 FT CYTOKINE; Granulocyte-macrophage colony-stimulating
 FT factor.
 FT NON_TER 144 144
 SQ SEQUENCE 144 AA; 16290 MW; ABAAD7633B580008 CRC64;
 Query Match 71.1%; Score 544; DB 2; Length 144;
 Best Local Similarity 79.5%; Pred. No. 1.3e-42;
 Matches 101; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 QY 16 APARSPSPQWHEVNAIQEARRLLNLSRDTAAENNEIVEISEMFDLQEPICLQTRLE 75
 DB 18 APTROPSPVTRPQHWDAIKEALSLNDSITDAVMDTEVVEVSEMFDSQEPICLQTRLE 77
 QY 76 LYKQGLRGLSTLTKGLPLTMASHYKHCPPTPTSCATQIITPESPKENLKDFLLVIFPD 135
 DB 78 LYKQGLRGLSTLTKGLPLTMASHYKHCPPTPTSCATQIITPESPKENLKDFLLVIFPD 137
 QY 136 CWEPVQK 142
 DB 138 CWEPVQK 144
 RESULT 7
 QY Q9MYK4 PRELIMINARY; PRT; 144 AA.
 AC Q9MYK4;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
 DE (Colony-stimulating factor) (CSF).
 GN Name-CSF2;
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervinae; Cervus.
 OX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lockhart E.A.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that stimulates the growth and differentiation
 of hematopoietic precursor cells from various lineages, including
 granulocytes, macrophages, eosinophils and erythrocytes (By
 similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -I- SIMILARITY: Belongs to the GM-CSF family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U14392; AAA21439.1; -.
CC HSSP: P04141; 2GMF.
CC InterPro: IPR009079; 4_helix_cytokine.
CC InterPro: IPR000773; GM-CSF.
CC Pfam: PF011109; GM-CSF; 1.
CC PRINTS; PR00693; GMCSFACTOR.
CC ProDom; PD007349; GM-CSF; 1.
CC SMART; SM00040; CSF2_1.
CC PROSITE; PS00702; GM-CSF; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 17
FT CHAIN 18 144
FT -----
FT DISULFID 71 113
FT DISULFID 105 138
FT CARBOHYD 44 44
FT CARBOHYD 54 54
FT SEQUENCE 144 AA; 16283 MW; 1F5FFD03C94394 CRC64;
SQ
Query Match 59.0%; Score 528; DB 1; Length 144;
Best Local Similarity 77.2%; Pred. No. 4.1e-41;
Matches 98; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQEPCLQTRLE 75
DB 18 APTROPSPVTRPQHVDAIKKLSLLNSSDSTAAMNETVEVSEFDDAEELTCLQTRLK 77
QY 76 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 135
DB 78 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 137
QY 136 CWEPVQE 142
DB 138 CWKPAQK 144
RESULT 8
ID Q8WN17 PRELIMINARY; PRT; 146 AA.
AC Q8WN17;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor (Fragment).
GN Name=GM-CSF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vecchione A., D'Mello F., Kanellos T.S., Howard C.R., Hamblin A.S.,
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448481; AAL41017.2; -.
DR HSSP; P04141; 2GMF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Pfam; PF01109; GM-CSF; 1.
DR PRINTS; PR00693; GMCSFACTOR.
DR ProDom; PD007349; GM-CSF; 1.
DR SMART; SM00040; CSF2; 1.
DR SEQUENCE 146 AA; 17173 MW; 75605CC1ADE9EFE9 CRC64;
Query Match 67.1%; Score 513; DB 2; Length 152;
Best Local Similarity 78.7%; Pred. No. 1.1e-39;
Matches 96; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQEPCLQTRLE 75
DB 18 APTROPSPVTRPQHVDAIKKLSLLNSSDSTAAMNETVEVSEFDDAEELTCLQTRLK 77
QY 76 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 135
DB 78 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 137
QY 136 CW 137
DB 138 CW 139
RESULT 10
ID CSF2_PIG STANDARD; PRT; 144 AA.
AC Q29118; Q29046;

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DR PROSITE; PS00702; GM-CSF; 1.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16604 MW; B92D0617F391281C CRC64;
Query Match 68.9%; Score 527; DB 2; Length 146;
Best Local Similarity 77.2%; Pred. No. 5.1e-41;
Matches 98; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQEPCLQTRLE 75
DB 18 APTROPSPVTRPQHVDAIKKLSLLNSSDSTAAMNETVEVSEFDDAEELTCLQTRLK 77
QY 76 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 135
DB 78 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 137
QY 136 CWEPVQE 142
DB 138 CWKPAQK 144
RESULT 9
ID Q95L10 PRELIMINARY; PRT; 152 AA.
AC Q95L10;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granulocyte-macrophage colony-stimulating-factor.
GN Name=GM-CSF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Maue S., Commandeur U., Steinbach F.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040203; AAK72108.2; -.
DR HSSP; P04141; 2GMF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000773; GM-CSF.
DR Pfam; PF01109; GM-CSF; 1.
DR PRINTS; PR00693; GMCSFACTOR.
DR ProDom; PD007349; GM-CSF; 1.
DR SMART; SM00040; CSF2; 1.
DR PROSITE; PS00702; GM-CSF; 1.
SQ SEQUENCE 152 AA; 17173 MW; 75605CC1ADE9EFE9 CRC64;
Query Match 67.1%; Score 513; DB 2; Length 152;
Best Local Similarity 78.7%; Pred. No. 1.1e-39;
Matches 96; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQEPCLQTRLE 75
DB 18 APTROPSPVTRPQHVDAIKKLSLLNSSDSTAAMNETVEVSEFDDAEELTCLQTRLK 77
QY 76 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 135
DB 78 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPTTSCATQIITFESPKENLKDFLLVIPD 137
QY 136 CW 137
DB 138 CW 139
RESULT 10
ID CSF2_PIG STANDARD; PRT; 144 AA.
AC Q29118; Q29046;

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DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
 DE (Colony-stimulating factor) (CSF).
 GN Name=CSF2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Foss D.L., Murtaugh M.P.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gloster S.E., Sandeman R.M., Strom A.D.G.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96167041; PubMed=8595928;
 RA Inumaru S., Takamatsu H.;
 RT "CDNA cloning of porcine granulocyte-macrophage colony-stimulating
 factor.";
 RL Immunol. Cell Biol. 73:474-476(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cho Y.W., Choi I.-S., Yoo H.S.;
 RT "Cloning of porcine granulocyte macrophage-colony stimulating factor
 in alveolar macrophages.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that stimulates the growth and differentiation
 CC of hematopoietic precursor cells from various lineages, including
 CC granulocytes, macrophages, eosinophils and erythrocytes (by
 CC similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the GM-CSF family.
 CC
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 CC
 DR EMBL; U61139; AAB03867.1; -;
 DR EMBL; U67318; AAB49939.1; -;
 DR EMBL; U67175; AAB06854.1; -;
 DR EMBL; D21074; BAA04649.1; -;
 DR EMBL; AV116504; AAM48280.1; -;
 DR HSSP; P04141; 2GMF.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR Pfam; PF01109; GM_CSF.
 DR PRINTS; PR00693; GMCSFACTOR.
 DR ProDom; PD007349; GM_CSF; 1.
 DR SMART; SM00040; CSF2; 1.
 DR PROSITE; PS00702; GM_CSF; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 144 Granulocyte-macrophage colony-stimulating factor.
 FT FT By similarity.
 FT DISULFID 71 113 By similarity.
 FT FT By similarity.
 FT CARBOHYD 105 138 N-linked (GlcNAc...) (Potential).
 FT FT N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 44 44 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 54 54 V -> I (in Ref. 2).
 FT CONFLICT 59 59 G -> E (in Ref. 2).
 FT CONFLICT 140 140
 FT CONFLICT 142 143 VK -> AQ (in Ref. 2).

SQ SEQUENCE 144 AA; 16254 MW; 793DACB62CF736D0 CRC64;
 Query Match 63.7%; Score 487; DB 1; Length 144;
 Best Local Similarity 70.1%; Pred. No. 2.6e-37;
 Matches 89; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
 QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDFAAEMNETVEVISEMFDLQEPCTCLQTRLE 75
 DB 18 APTRPSPVTRPQHWDAIKKALSLNNSNDFAAVNNEIVDVVCEMFDQEPCTCQTRLN 77
 QY 76 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPETSCTAQIITFESFKENLKDPLVIPFD 135
 DB 78 LYKQGLRGLSLTKLKSPLTLAKHYEQHCPLTETSCETQSIITFKSFKDLSNKLFLTIIPD 137
 QY 136 CWEPVQE 142
 DB 138 CWGPVKK 144
 RESULT 11
 Q6Q8A7 PRELIMINARY; PRT; 143 AA.
 AC Q6Q8A7;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Granulocyte macrophage colony stimulating factor.
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 OX NCBI_TaxID=89462;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dhinakar Raj G., HariShankar M., Thennarasu S., Mahalinga Nainar A.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY553190; AAS59070.1; -;
 DR GO; GO:0005129; F:granulocyte macrophage colony-stimulating f...; IEA.
 DR GO; GO:0005955; P:immune response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000773; GM_CSF.
 DR Pfam; PF01109; GM_CSF; 1.
 DR PRINTS; PR00693; GMCSFACTOR.
 DR ProDom; PD007349; GM_CSF; 1.
 DR SMART; SM00040; CSF2; 1.
 DR PROSITE; PS00702; GM_CSF; 1.
 SQ SEQUENCE 143 AA; 16105 MW; 274532FF0F0FE4C3F CRC64;
 Query Match 63.6%; Score 486.5; DB 2; Length 143;
 Best Local Similarity 70.1%; Pred. No. 2.9e-37;
 Matches 89; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
 QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDFAAEMNETVEVISEMFDLQEPCTCLQTRLE 75
 DB 18 APTRPSPVTRPQHWDAIKKALSLNNSNDFAAVNNEIVDVVCEMFDQEPCTCQTRLK 76
 QY 76 LYKQGLRGLSLTKLKGPLTMASHYKQHCPTPETSCTAQIITFESFKENLKDPLVIPFD 135
 DB 77 LYKQGLRGLSLTSLMGLSLTMATHYKHCPTPETSCTAQIITFKSFKEDLKEFLTIIPD 136
 QY 136 CWEPVQE 142
 DB 137 CWEPQAK 143
 RESULT 12
 CSF2_BOVIN STANDARD; PRT; 143 AA.
 ID CSF2_BOVIN
 AC P11052;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
 DE (Colony-stimulating factor) (CSF).
 GN Name=CSF2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=89096971; PubMed=3062386; DOI=10.1016/0161-5890(88)90120-4;
 RX Mallatzevski C.R., Schoenborn M.A., Cerretti D.P., Wignall J.M.,
 RA Picha K.S., Cosman D., Tushinski R.J., Gillis S., Baker P.E.,
 RT "Bovine GM-CSF: molecular cloning and biological activity of the
 RT recombinant protein.";
 RL Mol. Immunol. 25:843-850(1988).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90021093; PubMed=2678728; DOI=10.1016/0165-2427(89)90036-6;
 RX Leong S.R., Flagg G.M., Lawman M.J.P., Gray P.W.;
 RA "Cloning and expression of the cDNA for bovine granulocyte-macrophage
 RT colony-stimulating factor.";
 RL Vet. Immunol. Immunopathol. 21:261-278(1989).
 CC -!- FUNCTION: Cytokine that stimulates the growth and differentiation
 CC of hematopoietic precursor cells from various lineages, including
 CC granulocytes, macrophages, eosinophils and erythrocytes (By
 CC similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GM-CSF family.
 CC
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 CC
 CC EMBL: U22385; AAA66075.1; -
 DR PIR: J0037; F0BOGM.
 DR HSSP: P04141; 2GMF.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR000773; GM_CSF.
 DR Pfam: PF01109; GM_CSF; 1.
 DR PRINTS: PR00693; GMCSPACTOR.
 DR ProDom: PD007349; GM_CSF; 1.
 DR SMART: SM00040; CSF2; 1.
 DR PROSITE: PS00702; GM_CSF; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 143
 FT Granulocyte-macrophage colony-stimulating
 FT factor.
 FT By similarity.
 FT DISULFID 70 112
 FT DISULFID 104 137
 FT By similarity.
 FT CARBOHYD 44 44
 FT CARBOHYD 54 54
 FT N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 143 AA; 16157 MW; 4A24E26A870A51EC CRC64;
 Query Match 62.8%; Score 480.5; DB 1; Length 143;
 Best Local Similarity 68.5%; Pred. No. 1e-36;
 Matches 87; Conservative 20; Mismatches 19; Indels 1; Gaps 1;
 QY 16 APARSPSPQPEHVNIAQEARLLNLSRDTAAENNETVEVISEMFDLQPTCLOTRLE 75
 DB 18 APTRPNTATRPQWDAIKKALSLNHSDDTAVMMDT-EVSEKFDSEPTCLOTRLK 76
 QY 76 LYKQGLRGSITLKGPLTMMASHYKQHCPTPTSCATQIITPESFKENLKDFLLVIPP 135
 DB 77 LYKNGLSITLMSGLTMMATHYKHCPTPTSCGTQIFSKNFKDLKEFLFIIPD 136
 QY 136 CWEPVQE 142
 |||||

Db 137 CWEPQAK 143
 RESULT 13
 CSF2 CANFA
 ID _CSF2 CANFA STANDARD; PRT; 144 AA.
 AC P48749;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
 DE (Colony-stimulating factor) (CSF).
 GN Name=CSF2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91329842; PubMed=1868252;
 RX Nash R.A., Schuening F., Appelbaum F.R., Hammond W.P., Boone T.,
 RA Morris C.F., Slichter S.J., Storb R.;
 RT "Molecular cloning and in vivo evaluation of canine granulocyte-
 RT macrophage colony-stimulating factor.";
 RL Blood 78:930-937(1991).
 CC -!- FUNCTION: Cytokine that stimulates the growth and differentiation
 CC of hematopoietic precursor cells from various lineages, including
 CC granulocytes, macrophages, eosinophils and erythrocytes (By
 CC similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GM-CSF family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: S49738; AAB19466.1; -
 DR PIR: A4936; A4936.
 DR HSSP: P04141; 2GMF.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR000773; GM_CSF.
 DR Pfam: PF01109; GM_CSF; 1.
 DR PRINTS: PR00693; GMCSPACTOR.
 DR ProDom: PD007349; GM_CSF; 1.
 DR SMART: SM00040; CSF2; 1.
 DR PROSITE: PS00702; GM_CSF; 1.
 DR Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 144
 FT Granulocyte-macrophage colony-stimulating
 FT factor.
 FT By similarity.
 FT DISULFID 71 113
 FT DISULFID 105 138
 FT By similarity.
 FT CARBOHYD 44 44
 FT N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 144 AA; 16137 MW; 6323807E1F1C6343 CRC64;
 Query Match 61.8%; Score 473; DB 1; Length 144;
 Best Local Similarity 68.5%; Pred. No. 5.2e-36;
 Matches 87; Conservative 19; Mismatches 21; Indels 0; Gaps 0;
 QY 16 APARSPSPQPEHVNIAQEARLLNLSRDTAAENNETVEVISEMFDLQPTCLOTRLE 75
 DB 18 APTRPNTATRPQWDAIKKALSLNHSDDTAVMMDT-EVSEKFDSEPTCLOTRLK 77
 QY 76 LYKQGLRGSITLKGPLTMMASHYKQHCPTPTSCATQIITPESFKENLKDFLLVIPP 135
 DB 78 LYKEGLQGSITLKNPLTMMANHYKQHCPTPTSPCATQINFKSPKENLKDFLENI 137
 QY 136 CWEPVQE 142
 |||||

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OM protein - protein search, using sw model

Run on: March 8, 2005, 15:55:38 ; Search time 164 Seconds
(without alignments)
334.878 Million cell updates/sec

Title: US-10-723-083-2

Perfect score: 765

Sequence: 1 MHHHHSSGIEGRMAPARS.....ENLKDLVLVPDCEPVOE 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred' No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	682	89.2	259	2	AAR79317 IL-3 cont
2	682	89.2	259	3	AAY53198 Human int
3	682	89.2	259	4	Aae13992 Myelopoie
4	682	89.2	259	5	Abg97765 Human Int
5	682	89.2	259	8	Adj14353 Chimera p
6	679	88.8	533	2	Aaw19763 p53-GW-CS
7	678	88.6	128	1	Aap90118 Synthetic
8	678	88.6	128	1	AAP90115 Synthetic
9	678	88.6	128	2	AAR79338 pMON13012
10	678	88.6	128	2	Aaw00103 Granulocy
11	678	88.6	128	3	AAY53217 Human G-C
12	678	88.6	128	4	AAE14011 Chemically
13	678	88.6	128	5	ABG97784 Human int
14	678	88.6	128	8	ADJ14372 Protein r
15	678	88.6	274	2	AAR79320 IL-3 cont
16	678	88.6	274	3	AAY53201 Human int
17	678	88.6	274	4	AAE13995 Myelopoie
18	678	88.6	274	5	ABG97768 Human Int
19	678	88.6	274	8	ADJ14356 Chimera p
20	678	88.6	301	2	AAR79318 IL-3 cont
21	678	88.6	301	3	AAY53199 Human int
22	678	88.6	301	4	AAE13993 Chemically
23	678	88.6	301	5	ABG97766 Human Int
24	676	88.4	523	3	AAY44994 HD70scFv-
25	675	88.2	712	8	ADL16720 Human stu

26	675	88.2	736	7	ADFI5029 Human alb
27	675	88.2	736	7	ADFI4935 Human alb
28	674.5	88.2	736	7	ADFI4936 Human alb
29	674	88.1	128	2	AAR03199 New human
30	673	88.0	127	2	AAR13215 Oxidised
31	673	88.0	127	2	AAR41540 r-h-GW-CS
32	673	88.0	127	3	AAY69025 Amino aci
33	673	88.0	127	4	AAE13117 Mature hu
34	673	88.0	127	5	ABB78399 Amino aci
35	673	88.0	127	7	ADF70845 Human mac
36	673	88.0	127	8	ADL88868 Human cyt
37	673	88.0	128	2	AAW00102 Granulocy
38	673	88.0	131	1	AAP70351 Sequence
39	673	88.0	131	5	ABB08135 Human GMC
40	673	88.0	131	5	ABG31632 Human gra
41	673	88.0	131	5	AAOI9090 Human gra
42	673	88.0	143	8	ADJ36195 Self-coal
43	673	88.0	144	1	AAP60418 Human gra
44	673	88.0	144	1	AAP70657 Sequence
45	673	88.0	144	2	AAR04098 Metapyroc

ALIGNMENTS

RESULT 1

AAR79317
ID AAR79317 standard; protein; 259 AA.

XX AAR79317;

XX AC

XX DT 25-AUG-1999 (first entry)

XX DE IL-3 containing fusion protein.

XX KW interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;

XX KW mutant; mutein; fusion protein.

XX OS Synthetic.

XX PN WO9521254-A1.

XX PD 10-AUG-1995.

XX PF 02-FEB-1995; 95WO-US001185.

XX PR 04-FEB-1994; 94US-00192325.

XX PA (SEAR) SEARLE & CO G D.

XX PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;

XX PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;

XX DR WPI; 1995-283774/37.

XX DR N-PSDB; AAQ97169.

XX PT Fusion proteins comprising a human interleukin-3 variant, a linker and

XX PT interleukin-3, a variant or a colony stimulating factor - useful to

XX PT increase haematopoietic cell prodn. in a mammal.

XX PS Claim 16; Page 86; 447pp; English.

XX CC A new fusion protein has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L
-R1 or R1-R1, in which R1 is a mutant or variant of human interleukin-3
(hIL-3) having the present generic sequence, R2 is a second colony
stimulating factor (CSF) including cytokine, lymphokine, interleukin,
haematopoietic growth factor or IL-3 variant, and L is a linker. The
present sequence corresponds to native hIL-3(1-133) in which 1-14 amino
acids may be deleted from the N-terminal, 1-15 amino acids can be deleted
from the C-terminal, and at least 4 and up to 44 amino acids in the
region 17-123 are different from those in the native protein. The fusion
protein is used to increase haematopoietic cell production. It is also
useful as an IL-3 antagonist or as a discrete antigenic fragment for

CC production of antibodies useful in immunoassays and immunotherapy.
 CC Antagonists are used to block the growth of certain cancer cells and in
 CC treatment of asthma. The fusion protein can also be used to stimulate
 CC bone marrow and blood cell activation and growth in vitro before infusion
 CC , and to treat diseases characterised by decreased levels of myeloid,
 CC erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic
 CC system. The protein has the usual activity of both its component
 CC proteins, but may have increased synergistic activity and reduced
 CC undesired side effects
 XX
 SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 2; Length 259;
 Best Local Similarity 97.0%; Pred. No. 2.2e-64;
 Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 SGIEGRMAPRSPSTQPEWHVNAIQEARRLLNLSRDTAENNEVEVISEMFDLQEPT 68
 DB 126 SGGGSMAPRSPSTQPEWHVNAIQEARRLLNLSRDTAENNEVEVISEMFDLQEPT 185
 QY 69 CLQTRLEYKQGLRGLSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLQDF 128
 DB 186 CLQTRLEYKQGLRGLSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLQDF 245
 QY 129 LLVIPDCWEPVQE 142
 DB 246 LLVIPDCWEPVQE 259

RESULT 2
 AA53198
 ID AAY53198 standard; protein; 259 AA.
 AC AAY53198;
 DT 19-MAY-2000 (first entry)
 XX Human interleukin-3 mutant containing fusion protein SEQ ID NO:141.
 DE Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;
 KW radiation therapy; chemotherapy; bone marrow suppressive drug;
 KW bone marrow activation; blood cell activation; blood transplant.
 XX Homo sapiens.
 OS Synthetic.
 XX US6022535-A.
 PN 08-FEB-2000.
 XX 06-JUN-1995; 95US-00469318.
 XX 04-FEB-1994; 94US-00192325.
 PR 02-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95US-00411795.
 XX (SEAR) SEARLE & CO G D.
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
 PI Paik K, Thomas JW, McKearn JP, Olins PO, Caparon MH;
 XX WPI; 2000-160368/14.
 XX Treating hematopoietic disorders with fusion proteins comprising mutated
 PT interleukin-3 fused with secondary colony stimulating factors or other
 PT interleukin-3 variants.
 XX Example 27; Col 71-72; 276pp; English.
 PS Methods have been developed for treating haematopoietic disorders with
 CC fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-

CC 3) variants or mutant proteins (muteins) fused with secondary colony
 CC stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
 CC and/or haematopoietic colony stimulating factors) or other interleukin-3
 CC variants with or without a linker. The methods may be used in vivo to
 CC treat haematopoietic disorders resulting from bacterial, viral and fungal
 CC infections, cancer radiation therapy, chemotherapy or bone marrow
 CC suppressive drugs. They may also be used in vitro to stimulate bone
 CC marrow and blood cell activation and growth prior to infusion of the bone
 CC marrow and blood transplants into patients. IL-3 is a haematopoietic
 CC growth factor which has the property of being able to promote the
 CC survival, growth and differentiation of haematopoietic cells. The fusion
 CC molecules are characterised by possessing the usual activity of both of
 CC their constituent peptides and further by having a biological or
 CC physiological activity greater than the additive function of the IL-3 or
 CC second CSF alone (i.e. the peptides act synergistically). Their activity
 CC may also be further enhanced by the mutations they comprise. The
 CC variations may further reduce undesirable side effects associated with IL
 CC -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 3; Length 259;
 Best Local Similarity 97.0%; Pred. No. 2.2e-64;
 Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 SGIEGRMAPRSPSTQPEWHVNAIQEARRLLNLSRDTAENNEVEVISEMFDLQEPT 68
 DB 126 SGGGSMAPRSPSTQPEWHVNAIQEARRLLNLSRDTAENNEVEVISEMFDLQEPT 185
 QY 69 CLQTRLEYKQGLRGLSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLQDF 128
 DB 186 CLQTRLEYKQGLRGLSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLQDF 245
 QY 129 LLVIPDCWEPVQE 142
 DB 246 LLVIPDCWEPVQE 259

RESULT 3
 AA531992
 ID AAE13992 standard; protein; 259 AA.
 XX AAE13992;
 XX 26-FEB-2002 (first entry)
 DT Myelopoietin (MPO) protein #127.
 XX Myelopoietin conjugate; MPO; immunosuppressive; vulnery; antiparasitic;
 KW antibacterial; virucide; interleukin-3; IL-3; haematopoietic disorder;
 KW haematopoietic growth factor receptor; neutropenia; thrombocytopenia;
 KW leukopenia; anaemia; chemotherapy; bone marrow transplantation; burn;
 KW radiation therapy; haematopoietic progenitor mobilisation; infection;
 XX wound healing.
 XX Unidentified.
 XX WO200176639-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-US011256.
 XX 06-APR-2000; 2000US-0195496P.
 XX (PHAA) PHARMACIA CORP.
 PA (FINN/) FINN R.
 PA (GOKA/) GOKARN Y.
 PA (HILL/) HILLS R.
 PA (NICA/) NICASTRO P.
 PA (QIHH/) QI H.
 PA (SEDO/) SEDO K.

PA (SIEG/) SIEGEL N.
 PI (WALT/) WALTER S.
 XX Finn R, Gokarn Y, Hills R, Nicastro P, Qi H, Sedo K, Siegel N;
 PI Walter S;
 XX WPI; 2001-657130/75.
 DR
 XX Myelopietin conjugate for treating e.g. leukopenia comprises a water-
 PT soluble polymer attached to the protein.
 XX
 PS Claim 5; Page 197-198; 429pp; English.
 XX
 CC The invention relates to chemically modified myelopietin (MPO)
 CC conjugates having at least one water-soluble polymer molecule covalently
 CC attached, via activating group, to at least one amino acid residue of a
 CC biologically active myelopietin polypeptide. MPOs are multifunctional
 CC agonists of human interleukin-3 (IL-3) and another haematopoietic growth
 CC factor receptor. Sequences of the invention are useful for treating
 CC haematopoietic disorders (e.g. neutropenia, leukopenia, thrombocytopenia
 CC and anaemia), including those arising from chemotherapy and radiation
 CC therapy. MPOs are also useful in bone marrow transplantation, wound
 CC healing, burn treatment and the treatment of parasite, bacterial or viral
 CC infection. They are useful for mobilising haematopoietic progenitors and
 CC stem cells. The chemically modified MPOs have a longer lasting neutrophil
 CC -releasing activity, decreased clearance rate, increased stability and
 CC decreased antigenicity than unmodified myelopietins. The present
 CC sequence is a myelopietin protein
 XX
 SQ Sequence 259 AA;
 Query Match 89.2%; Score 682; DB 4; Length 259;
 Best Local Similarity 97.0%; Pred. No. 2.2e-64;
 Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 9 SGIEGRMAPRSPSPSTQPMWVHNAIQEARLLNLSRDTAENNETVEVISEMFDLOEPT 68
 DB 126 SGGGNNAPRSPSPSTQPMWVHNAIQEARLLNLSRDTAENNETVEVISEMFDLOEPT 185
 QY 69 CLQTRLELYKQGLRSLTKLKGPLTWASHYKHQCPTPTSCATQIITPESKFNKDF 128
 DB 186 CLQTRLELYKQGLRSLTKLKGPLTWASHYKHQCPTPTSCATQIITPESKFNKDF 245
 QY 129 LLVIPDCWEPVQE 142
 DB 246 LLVIPDCWEPVQE 259
 RESULT 4
 ABG97765
 ID ABG97765 standard; protein; 259 AA.
 XX
 AC ABG97765;
 XX
 DT 18-DEC-2002 (first entry)
 XX
 DE Human Interleukin-3 chimaeric protein #20.
 XX
 KW Human; interleukin-3; IL-3; mutant; mutagen; stem cell;
 KW haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; G-CSF;
 KW G-CSFser17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
 KW human growth hormone; B-cell growth factor; leukaemia;
 KW B-cell differentiation factor; eosinophil differentiation factor;
 KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
 KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
 KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
 KW myelofibrosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX US6436387-B1.
 PN
 XX

PD 20-AUG-2002.
 XX
 PF 09-DEC-1996; 96US-00762227.
 XX
 PR 24-NOV-1992; 92US-00981044.
 XX
 PR 22-NOV-1993; 93WO-US011197.
 PR 04-FEB-1994; 94US-00192325.
 PR 04-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95US-00411795.
 PR 06-JUN-1995; 95US-00446872.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, McKearn JP, Ollins PO, Paik K, Thomas JW;
 XX WPI; 2002-749206/81.
 XX
 XX Ex vivo expansion of stem cells, for enhancing transduction efficiency of
 PT cultured stem cells, comprises culturing stem cells in growth medium
 PT having mutant interleukin-3, and hematopoietic factor, and harvesting
 PT cultured cells.
 XX
 PS Claim 8; Col 247-250; 203pp; English.
 XX
 CC The invention relates to ex vivo expansion of stem cells, comprises
 CC culturing stem cells with a growth medium comprising a chimaera protein,
 CC and harvesting the cultured stem cells. The chimaera is based on a
 CC mutated human interleukin-3 (IL-3) sequence coupled to a haematopoietic
 CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
 CC CSFser17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
 CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
 CC differentiation factor, eosinophil differentiation factor and stem cell
 CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
 CC in the specification. Also included is a method for enhancing the
 CC efficiency of the transduction of cultured stem cells by a heterologous
 CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
 CC culturing the stem cells with a growth medium comprising the transduced
 CC transducing DNA into cultured cells; and (d) harvesting the transduced
 CC cells. The method is useful for ex vivo expansion of stem cells, and
 CC enhancing the efficiency of the transduction of cultured stem cells by a
 CC heterologous gene. The method is also useful for treating a patient
 CC having a haematopoietic disorder. The expanded haematopoietic cells are
 CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
 CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
 CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
 CC and myelofibrosis. The present sequence is a human IL-3
 CC mutant/haematopoietic factor chimaeric sequence
 XX
 SQ Sequence 259 AA;
 Query Match 89.2%; Score 682; DB 5; Length 259;
 Best Local Similarity 97.0%; Pred. No. 2.2e-64;
 Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 9 SGIEGRMAPRSPSPSTQPMWVHNAIQEARLLNLSRDTAENNETVEVISEMFDLOEPT 68
 DB 126 SGGGNNAPRSPSPSTQPMWVHNAIQEARLLNLSRDTAENNETVEVISEMFDLOEPT 185
 QY 69 CLQTRLELYKQGLRSLTKLKGPLTWASHYKHQCPTPTSCATQIITPESKFNKDF 128
 DB 186 CLQTRLELYKQGLRSLTKLKGPLTWASHYKHQCPTPTSCATQIITPESKFNKDF 245
 QY 129 LLVIPDCWEPVQE 142
 DB 246 LLVIPDCWEPVQE 259
 RESULT 5
 ADJ14353
 ID ADJ14353 standard; protein; 259 AA.
 XX
 AC ADJ14353;
 XX


```
Matches 128; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 12 EGMAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEVISEMFDLQPTCLQ 71
Db : |||||
393 DRSAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEVISEMFDLQPTCLQ 452
QY 72 TRLELYKQGLRGLSLTKLKGPLTWMAHYKHQCHPPTPETSATQIITFESFKENLKDPLLV 131
Db |||||
453 TRLELYKQGLRGLSLTKLKGPLTWMAHYKHQCHPPTPETSATQIITFESFKENLKDPLLV 512
QY 132 IPFDCWEPVOE 142
Db |||||
513 IPFDCWEPVOE 523

RESULT 7
AAP90118
ID AAP90118 standard; protein; 128 AA.
XX
AC AAP90118;
XX
XX 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
XX Synthetic human granulocyte colony stimulating factor.
XX
XX BspMI; restriction sites; blunt ends; fusion proteins; synthetic;
KW human granulocyte colony stimulating factor.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX GB2212160-A.
PN
XX 19-JUL-1989.
PD
XX 13-NOV-1987; 87GB-00726581.
PF
XX 13-NOV-1987; 87GB-00026581.
PR
XX (BRBI-) BRITISH BIO-TECHN L.
PA
XX Edwards RM;
PI
XX
XX WPI; 1989-208959/29.
DR
XX N-PSDB; AAN90383.
XX
XX DNA including recognition site for BspMI enzyme - allowing generation of
PT blunt end for fusion in prodn. of fusion proteins.
PT
XX
XX Disclosure; Fig 2; 23pp; English.
PS
XX Synthetic human granulocyte colony stimulating factor (GM-CSF) contg.
CC useful restriction sites, and a BspMI site. See corresp. AAN90383. Its
CC DNA is useful for generating blunt ends in fusion protein prodn. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 128 AA;
SQ

Query Match 88.6%; Score 678; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 MAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEVISEMFDLQPTCLQTRL 74
Db |||||
1 MAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEVISEMFDLQPTCLQTRL 60
QY 75 ELYKQGLRGLSLTKLKGPLTWMAHYKHQCHPPTPETSATQIITFESFKENLKDPLLVIPF 134
Db |||||
61 ELYKQGLRGLSLTKLKGPLTWMAHYKHQCHPPTPETSATQIITFESFKENLKDPLLVIPF 120
QY 135 DCWEPVOE 142
Db |||||
121 DCWEPVOE 128

RESULT 9
AAR79338
ID AAR79338 standard; protein; 128 AA.
XX
AC AAR79338;
XX
```

```
|||||
Db 121 DCWEPVOE 128

RESULT 8
AAP90115
ID AAP90115 standard; protein; 128 AA.
XX
XX AAP90115;
XX
XX 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
XX Synthetic human granulocyte colony stimulating factor.
XX
XX Human granulocyte colony stimulating factor; Synthetic restriction sites;
KW cassette mutagenesis; GM-CSF; expression system.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX GB2212159-A.
PN
XX 19-JUL-1989.
PD
XX 13-NOV-1987; 87GB-00026580.
PF
XX 13-NOV-1987; 87GB-00026580.
PR
XX (BRBI-) BRITISH BIO-TECHN L.
PA
XX Edwards RM;
PI
XX
XX WPI; 1989-208958/29.
DR
XX
XX Human granulocyte-macrophage colony stimulating factor - synthetic DNA
PT includes restriction sites for cassette mutagenesis and incorporation in
PT expression systems.
XX
XX Claim 2; Fig 3a; 21pp; English.
PS
XX Synthetic human granulocyte colony stimulating factor (GM-CSF), see
CC corresp. AAN90274. Its DNA has useful restriction sites for: HindIII;
CC BspMI; NcoI; BstEII; BsmI; EcoRV; BglI; ApaI; BclI; XbaI; BamHI; and
CC EcoRI. Used to facilitate cassette mutagenesis of selected regions.
CC Synthesised by phosphoramidite chemistry, by dividing desired gene into
CC 18 oligomers. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 128 AA;
SQ

Query Match 88.6%; Score 678; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 MAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEVISEMFDLQPTCLQTRL 74
Db |||||
1 MAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEVISEMFDLQPTCLQTRL 60
QY 75 ELYKQGLRGLSLTKLKGPLTWMAHYKHQCHPPTPETSATQIITFESFKENLKDPLLVIPF 134
Db |||||
61 ELYKQGLRGLSLTKLKGPLTWMAHYKHQCHPPTPETSATQIITFESFKENLKDPLLVIPF 120
QY 135 DCWEPVOE 142
Db |||||
121 DCWEPVOE 128

RESULT 9
AAR79338
ID AAR79338 standard; protein; 128 AA.
XX
AC AAR79338;
XX
```

DT 25-AUG-1999 (first entry)
 XX pMON13012 peptide.
 DE Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
 XX mutant; mutein; fusion protein.
 KW Synthetic.
 XX Homo sapiens.
 OS WO9521254-A1.
 XX 10-AUG-1995.
 PD 02-FEB-1995; 95WO-US001185.
 PF 04-FEB-1994; 94US-00192325.
 XX (SEAR) SEARLE & CO G D.
 PA Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
 DR WPI; 1995-283774/37.
 DR N-PSDB; AAQ97208.
 XX Fusion proteins comprising a human interleukin-3 variant, a linker and
 PT interleukin-3, a variant or a colony stimulating factor - useful to
 PT increase haematopoietic cell prodn. in a mammal.
 XX Example 20; Page 125; 447pp; English.
 PS A new fusion protein disclosed which has the formula R1-L-R2, R2-L-R1,
 XX R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
 CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
 CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
 CC or IL-3 variant, and L is a linker. Generic sequences are described in
 CC AA003235 - AA003242, and specifically claimed examples are shown in
 CC AA079298-R79335 and AA079342-R79345. The fusion protein is made by
 CC recombinant DNA techniques. Specifically claimed examples of DNA
 CC sequences which encode these proteins are shown in AAQ97167-Q97204 and
 CC AAQ97222-Q97227. The fusion protein is used to increase haematopoietic
 CC cell production. It is also useful as an IL-3 antagonist or as a discrete
 CC antigenic fragment for production of antibodies useful in immunoassays
 CC and immunotherapy. Antagonists are used to block the growth of certain
 CC cancer cells and in treatment of asthma. The fusion protein can also be
 CC used to stimulate bone marrow and blood cell activation and growth in
 CC vitro before infusion, and to treat diseases characterized by decreased
 CC levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the
 CC haematopoietic system. The protein has the usual activity of both its
 CC component proteins, but may have increased synergistic activity and
 CC reduced undesired side effects
 XX Sequence 128 AA;
 SQ Query Match 88.6%; Score 678; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.3e-64;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEISEMFDLQEPCTCLOTRL 74
 DB 1 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEISEMFDLQEPCTCLOTRL 60
 QY 75 ELYKQGLRGLSTKLKGLPTWASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 134
 DB 61 ELYKQGLRGLSTKLKGLPTWASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 120
 QY 135 DCWEPVQE 142
 DB 121 DCWEPVQE 128
 RESULT 11
 ID AAY53217
 XX AAY53217 standard; protein; 128 AA.
 XX AAY53217;
 XX AC
 XX DT 19-MAY-2000 (first entry)
 XX Human G-CSF mutant protein sequence SEQ ID NO:160.
 DE Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;

AAW00103
 ID AAW00103 standard; protein; 128 AA.
 XX AAW00103;
 AC AAW00103;
 XX 25-MAR-2003 (revised)
 DT 11-FEB-1997 (first entry)
 XX Granulocyte macrophage colony-stimulating factor (ilei01).
 DE GM-CSF; granulocyte macrophage colony-stimulating factor; expression;
 KW construct; stable; production.
 KW Homo sapiens.
 OS JP08173185-A.
 XX 09-JUL-1996.
 PD 28-APR-1987; 95JP-00263370.
 PF 28-APR-1987; 87JP-00106148.
 PR (AMGE-) AMGEN INC.
 XX (KIRI) KIRIN BREWERY KK.
 PA WPI; 1996-365600/37.
 DR N-PSDB; AAT34400.
 XX Prodn. of human granulocyte macrophage colony-stimulating factor - by
 PT culturing E. coli transformed with human GM-CSF DNA.
 XX Claim 1; Page 2; 16pp; Japanese.
 PS The present sequence is that of human granulocyte macrophage colony-
 CC stimulating factor (hGM-CSF; n = 101, Ile). A series of oligonucleotides
 CC were synthesised and ligated together to form a stable expression
 CC construct. The technique is used for the efficient prodn. of a
 CC glycoprotein with hGM-CSF activity. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX Sequence 128 AA;
 SQ Query Match 88.6%; Score 678; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.3e-64;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEISEMFDLQEPCTCLOTRL 74
 DB 1 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEISEMFDLQEPCTCLOTRL 60
 QY 75 ELYKQGLRGLSTKLKGLPTWASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 134
 DB 61 ELYKQGLRGLSTKLKGLPTWASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 120
 QY 135 DCWEPVQE 142
 DB 121 DCWEPVQE 128
 RESULT 11
 ID AAY53217
 XX AAY53217 standard; protein; 128 AA.
 XX AAY53217;
 XX AC
 XX DT 19-MAY-2000 (first entry)
 XX Human G-CSF mutant protein sequence SEQ ID NO:160.
 DE Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;

KW radiation therapy; chemotherapy; bone marrow suppressive drug;
 KW bone marrow activation; blood cell activation; blood transplant.
 XX
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US6022535-A.
 XX
 PD 08-FEB-2000.
 XX
 PD 06-JUN-1995; 95US-00469318.
 XX
 XX 04-FEB-1994; 94US-00192325.
 PR 02-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95WO-00411795.
 XX
 XX (SEAR) SEARLE & CO G D.
 XX
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
 PI Paik K, Thomas JW, Mckearn JP, Olins PO, Caparon MH;
 XX
 XX WPI; 2000-160368/14.
 XX
 XX Treating hematopoietic disorders with fusion proteins comprising mutated
 PT interleukin-3 fused with secondary colony stimulating factors or other
 PT interleukin-3 variants.
 XX
 XX Example 20; Col 109-111; 276pp; English.
 XX
 XX Methods have been developed for treating hematopoietic disorders with
 CC fusion proteins comprising recombinant, mutated human interleukin-3 (IL-
 CC 3) variants or mutant proteins (mutins) fused with secondary colony
 CC stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
 CC and/or hematopoietic colony stimulating factors) or other interleukin-3
 CC variants with or without a linker. The methods may be used in vivo to
 CC treat hematopoietic disorders resulting from bacterial, viral and fungal
 CC infections, cancer radiation therapy, chemotherapy or bone marrow
 CC suppressive drugs. They may also be used in vitro to stimulate bone
 CC marrow and blood cell activation and growth prior to infusion of the bone
 CC marrow and blood transplants into patients. IL-3 is a hematopoietic
 CC growth factor which has the property of being able to promote the
 CC survival, growth and differentiation of hematopoietic cells. The fusion
 CC molecules are characterised by possessing the usual activity of both of
 CC their constituent peptides and further by having a biological or
 CC physiological activity greater than the additive function of the IL-3 or
 CC second CSF alone (i.e. the peptides act synergistically). Their activity
 CC may also be further enhanced by the mutations they comprise. The
 CC variations may further reduce undesirable side effects associated with IL
 CC -3. AAY3130 to AAY3226, and AAA03721 to AAA03782 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 128 AA;

Query Match 88.6%; Score 678; DB 3; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.3e-64;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQWEHVNAIQEARLLNLSRDTAAENNETVEISEMFDLQETCLQTRL 74

DB 1 MAPARSPSPSTQWEHVNAIQEARLLNLSRDTAAENNETVEISEMFDLQETCLQTRL 60

QY 75 ELYKQGLRGLSLTKLKGPLTWASHYKQHCPTTSCATQIITFESFKENLKDPLLVIPF 134

DB 61 ELYKQGLRGLSLTKLKGPLTWASHYKQHCPTTSCATQIITFESFKENLKDPLLVIPF 120

QY 135 DCWEPVQE 142

DB 121 DCWEPVQE 128

RESULT 12

AAE14011

ID AAE14011 standard; protein; 128 AA.

XX
 AC AAE14011;

26-FEB-2002 (first entry)

Chemically modified myelopoietin (MPO) conjugate related protein #11.

Myelopoietin conjugate; MPO; immunosuppressive; vulnery; antiparasitic;
 antibacterial; virucide; interleukin-3; IL-3; hematopoietic disorder;
 hematopoietic growth factor receptor; neutropenia; thrombocytopenia;
 leukopenia; anaemia; chemotherapy; bone marrow transplantation; burn;
 radiation therapy; hematopoietic progenitor mobilisation; infection;
 wound healing.

Unidentified.

WO200176639-A2.

18-OCT-2001.

06-APR-2001; 2001WO-US011256.

06-APR-2000; 2000US-0195496P.

(PHAA) PHARMACIA CORP.

(FINN/) FINN R.

(GOKA/) GOKARN Y.

(HILL/) HILLS R.

(NICA/) NICASTRO P.

(QIHH/) QI H.

(SEDO/) SEDO K.

(SIEG/) SIEGEL N.

(WALT/) WALTER S.

Finn R, Gokarn Y, Hills R, Nicastro P, Qi H, Sado K, Siegel N;

Walter S;

WPI; 2001-657130/75.

Myelopoietin conjugate for treating e.g. leukopenia comprises a water-

soluble polymer attached to the protein.

Disclosure; Page 215; 429pp; English.

The invention relates to chemically modified myelopoietin (MPO)
 conjugates having at least one water-soluble polymer molecule covalently
 attached, via activating group, to at least one amino acid residue of a
 biologically active myelopoietin polypeptide. MPOs are multifunctional
 agonists of human interleukin-3 (IL-3) and another hematopoietic growth
 factor receptor. Sequences of the invention are useful for treating
 hematopoietic disorders (e.g. neutropenia, leukopenia, thrombocytopenia
 and anaemia), including those arising from chemotherapy and radiation
 therapy. MPOs are also useful in bone marrow transplantation, wound
 healing, burn treatment and the treatment of parasite, bacterial or viral
 infection. They are useful for mobilising hematopoietic progenitors and
 stem cells. The chemically modified MPOs have a longer lasting neutrophil
 releasing activity, decreased clearance rate, increased stability and
 decreased antigenicity than unmodified myelopoietins. The present
 sequence is a chemically modified myelopoietin conjugate related protein

Sequence 128 AA;

Query Match 88.6%; Score 678; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 2.3e-64;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQWEHVNAIQEARLLNLSRDTAAENNETVEISEMFDLQETCLQTRL 74

DB 1 MAPARSPSPSTQWEHVNAIQEARLLNLSRDTAAENNETVEISEMFDLQETCLQTRL 60

QY 75 ELYKQGLRGLSLTKLKGPLTWASHYKQHCPTTSCATQIITFESFKENLKDPLLVIPF 134

DB 61 ELYKQGLRGLSLTKLKGPLTWASHYKQHCPTTSCATQIITFESFKENLKDPLLVIPF 120

QY 135 DCWEPVQE 142
 Db 121 DCWEPVQE 128

RESULT 13
 ABG97784
 ID ABG97784 standard; protein; 128 AA.
 AC ABG97784;
 XX
 XX
 DT 18-DEC-2002 (first entry)
 DE Human Interleukin-3 chimaeric protein #39.
 KW Human; interleukin-3; IL-3; mutant; mutein; stem cell;
 KW haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; G-CSF;
 KW G-CSFser17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
 KW human growth hormone; B-cell growth factor; leukaemia;
 KW B-cell differentiation factor; eosinophil differentiation factor;
 KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
 KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
 KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
 KW myelofibrosis.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX US6436387-B1.
 XX
 XX 20-AUG-2002.
 PD
 XX
 XX 09-DEC-1996; 96US-00762227.
 PF
 XX
 XX 24-NOV-1992; 92US-00981044.
 PR
 XX 22-NOV-1993; 93WO-US011197.
 PR
 XX 04-FEB-1994; 94US-00192325.
 PR
 XX 04-FEB-1995; 95WO-US001185.
 PR
 XX 06-APR-1995; 95US-00411795.
 PR
 XX 06-JUN-1995; 95US-00446872.
 PR
 XX (SEAR) SEARLE & CO G D.
 PA
 XX
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;
 XX
 XX WPI; 2002-749206/81.
 XX
 XX Ex vivo expansion of stem cells, for enhancing transduction efficiency of
 PT cultured stem cells, comprises culturing stem cells in growth medium
 PT having mutant interleukin-3, and hematopoietic factor, and harvesting
 PT cultured cells.
 XX
 XX Claim 8; Col 283-284; 203pp; English.
 PS
 XX The invention relates to ex vivo expansion of stem cells, comprises
 CC culturing stem cells with a growth medium comprising a chimaera protein,
 CC and harvesting the cultured stem cells. The chimaera is based on a
 CC mutated human interleukin-3 (IL-3) sequence coupled to a haematopoietic
 CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
 CC CSFser17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
 CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
 CC differentiation factor, eosinophil differentiation factor and stem cell
 CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
 CC in the specification. Also included is a method for enhancing the
 CC efficiency of the transduction of cultured stem cells by a heterologous
 CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
 CC culturing the stem cells with a growth medium comprising the chimaera (c)
 CC transducing DNA into cultured cells; and (d) harvesting the transduced
 CC cells. The method is useful for ex vivo expansion of stem cells, and
 CC enhancing the efficiency of the transduction of cultured stem cells by a
 CC heterologous gene. The method is also useful for treating a patient

CC having a haematopoietic disorder. The expanded haematopoietic cells are
 CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
 CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
 CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
 CC and myelofibrosis. The present sequence is a human IL-3
 CC mutant/haematopoietic factor chimaeric sequence
 XX
 XX Sequence 128 AA;
 QY Query Match 88.6%; Score 678; DB 5; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2.3e-64; Indels 0; Gaps 0;
 Matches 128; Conservative 0; Mismatches 0;
 QY 15 MAPARSPSPSTQWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQPTCLQTRL 74
 Db 1 MAPARSPSPSTQWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQPTCLQTRL 60
 QY 75 ELYKQGLRSLTKLKGPLTMASHYKQHCPPPTSCATQIITFESFKENLKDFLLVIPP 134
 Db 61 ELYKQGLRSLTKLKGPLTMASHYKQHCPPPTSCATQIITFESFKENLKDFLLVIPP 120
 QY 135 DCWEPVQE 142
 Db 121 DCWEPVQE 128

RESULT 14
 ADJ14372
 ID ADJ14372 standard; protein; 128 AA.
 XX
 AC ADJ14372;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX
 DE Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 140.
 KW stem cell; antianaemic; immunostimulant; immunomodulator;
 KW antiinflammatory; dermatologic; immunosuppressive; cytostatic;
 KW neuroprotective; haematopoietic disorder; gene therapy; myeloid; erythroid;
 KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
 KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
 KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3.
 XX
 OS Unidentified.
 OS
 XX US2003185790-A1.
 XX
 XX 02-OCT-2003.
 PD
 XX
 XX 26-FEB-2002; 2002US-00083446.
 PF
 XX 24-NOV-1992; 92US-00981044.
 PR
 XX 22-NOV-1993; 93WO-US011197.
 PR
 XX 04-FEB-1994; 94US-00192325.
 PR
 XX 02-FEB-1995; 95WO-US001185.
 PR
 XX 06-APR-1995; 95US-00411795.
 PR
 XX 06-JUN-1995; 95US-00446872.
 PR
 XX 09-DEC-1996; 96US-00762227.
 XX
 XX (BAUE/) BAUER S C.
 PA (ABRA/) ABRAMS M A.
 PA (BRAP/) BRAFORD-GOLDBERG S R.
 PA (CAPA/) CAPARON M H.
 PA (EAST/) EASTON A M.
 PA (KLEI/) KLEIN B K.
 PA (MCKE/) MCKEARN J P.
 PA (OLIN/) OLINS P O.
 PA (PAIK/) PAIK K.
 PA (THOM/) THOMAS J W.
 XX
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;
 XX

DR WPI; 2004-096775/10.

XX Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating

PT aplastic anemia, involves culturing the stem cells with growth medium

PT comprising chimera protein, and harvesting the cultured stem cells.

XX

PS Disclosure; SEQ ID NO 160; 202pp; English.

XX

CC The invention relates to a novel method whereby stem cells are ex vivo

CC expanded via culturing the stem cells with a growth medium comprising a

CC chimera protein, followed by harvesting of the cultured stem cells. The

CC method of the invention has antianemic, immunostimulant,

CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,

CC cytostatic and neuroprotective applications and may be useful to target

CC hematopoietic cells for gene therapy, preferably for treating patients

CC having a haemopoietic disorder characterised by decreased levels of

CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic

CC system. The expanded ex vivo cells may be used to treat neutropenia,

CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,

CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or

CC myelofibrosis. The current sequence is that of a protein related to the

CC human interleukin-3 (IL-3) mutant protein of the invention.

XX

SQ Sequence 128 AA;

Query Match 88.6%; Score 678; DB 8; Length 128;

Best Local Similarity 100.0%; Pred. No. 2.3e-64;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 74

DB 1 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 60

QY 75 ELYKQGLRGLSLTKLKGPLTMMASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 134

DB 61 ELYKQGLRGLSLTKLKGPLTMMASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 120

QY 135 DCWEPVQE 142

DB 121 DCWEPVQE 128

RESULT 15

AAR79320

ID AAR79320 standard; protein; 274 AA.

XX

AC AAR79320;

XX

DT 25-AUG-1999 (first entry)

XX

DE IL-3 containing fusion protein.

XX

KW interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;

KW mutant; mutein; fusion protein.

XX

OS Synthetic.

XX

PN WO9521254-A1.

XX

PD 10-AUG-1995.

XX

PF 02-FEB-1995; 95WO-US0001185.

XX

PR 04-FEB-1994; 94US-00192325.

XX

PA (SEAR) SEARLE & CO G D.

XX

PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;

PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;

XX

DR WPI; 1995-283774/37.

DR N-PSDB; AAQ97183.

XX

PT Fusion proteins comprising a human interleukin-3 variant, a linker and

PT interleukin-3, a variant or a colony stimulating factor - useful to

XX increase haematopoietic cell prodn. in a mammal.

PS Claim 16; Page 87-88; 447pp; English.

XX

CC A new fusion protein has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L

CC -R1 or R1-R1, in which R1 is a mutant or variant of human interleukin-3

CC (hIL-3) having the present generic sequence, R2 is a second colony

CC stimulating factor (CSF) including cytokine, lymphokine, interleukin,

CC haematopoietic growth factor or IL-3 variant, and L is a linker. The

CC present sequence corresponds to native hIL-3(1-133) in which 1-14 amino

CC acids may be deleted from the N-terminal, 1-15 amino acids can be deleted

CC from the C-terminal, and at least 4 and up to 44 amino acids in the

CC region 17-123 are different from those in the native protein. The fusion

CC protein is used to increase haematopoietic cell production. It is also

CC useful as an IL-3 antagonist or as a discrete antigenic fragment for

CC production of antibodies useful in immunoassays and immunotherapy.

CC Antagonists are used to block the growth of certain cancer cells and in

CC treatment of asthma. The fusion protein can also be used to stimulate

CC bone marrow and blood cell activation and growth in vitro before infusion

CC ; and to treat diseases characterised by decreased levels of myeloid,

CC erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic

CC system. The protein has the usual activity of both its component

CC proteins, but may have increased synergistic activity and reduced

CC undesired side effects

XX

SQ Sequence 274 AA;

Query Match 88.6%; Score 678; DB 2; Length 274;

Best Local Similarity 100.0%; Pred. No. 6.4e-64;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 74

DB 147 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 206

QY 75 ELYKQGLRGLSLTKLKGPLTMMASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 134

DB 207 ELYKQGLRGLSLTKLKGPLTMMASHYKQHCPTPTSCATQIITFESFKENLKDPLLVIPF 266

QY 135 DCWEPVQE 142

DB 267 DCWEPVQE 274

Search completed: March 8, 2005, 16:10:22

Job time : 167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 16:13:34 ; Search time 131 Seconds
(without alignments)
356.675 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHSSGIEGRMAPARS.....ENLKDPLLVPDCWEPQVE 142

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	89.2	259	14	US-10-083-446-141 Sequence 141, App
2	678	88.6	128	14	US-10-083-446-160 Sequence 160, App
3	678	88.6	274	14	US-10-083-446-144 Sequence 144, App
4	678	88.6	301	14	US-10-083-446-142 Sequence 142, App
5	675	88.2	712	15	US-10-609-346-10 Sequence 10, Appl
6	673	88.0	127	9	US-09-821-883-18 Sequence 18, Appl
7	673	88.0	127	9	US-09-800-016-1 Sequence 1, Appl
8	673	88.0	127	9	US-09-792-793A-15 Sequence 15, Appl
9	673	88.0	127	14	US-10-400-377-8 Sequence 8, Appl
10	673	88.0	127	14	US-10-400-708-8 Sequence 8, Appl
11	673	88.0	127	14	US-10-298-148-8 Sequence 8, Appl
12	673	88.0	127	15	US-10-375-209A-15 Sequence 15, Appl
13	673	88.0	127	16	US-10-658-834A-202 Sequence 202, App

14 673 88.0 127 16 US-10-743-295-5 Sequence 5, Appli
15 673 88.0 127 16 US-10-773-939-8 Sequence 8, Appli
16 673 88.0 127 16 US-10-774-149-8 Sequence 8, Appli
17 673 88.0 143 5 US-10-449-831A-142 Sequence 142, App
18 673 88.0 144 9 US-09-923-246-114 Sequence 114, App
19 673 88.0 144 14 US-10-295-723-114 Sequence 114, App
20 673 88.0 144 14 US-10-282-622-10 Sequence 10, Appl
21 673 88.0 144 14 US-10-131-985-15 Sequence 15, Appl
22 673 88.0 144 15 US-10-116-275-217 Sequence 217, App
23 673 88.0 144 15 US-10-456-780-10 Sequence 10, Appl
24 673 88.0 144 15 US-10-411-037-18 Sequence 18, Appl
25 673 88.0 144 15 US-10-609-346-20 Sequence 20, Appl
26 673 88.0 144 15 US-10-411-026-18 Sequence 18, Appl
27 673 88.0 144 15 US-10-447-315-19 Sequence 19, Appl
28 673 88.0 144 15 US-10-410-962-18 Sequence 18, Appl
29 673 88.0 144 15 US-10-411-049-18 Sequence 18, Appl
30 673 88.0 144 16 US-10-659-684-114 Sequence 114, App
31 673 88.0 144 16 US-10-410-930-18 Sequence 18, Appl
32 673 88.0 144 16 US-10-410-997-18 Sequence 18, Appl
33 673 88.0 144 16 US-10-411-042-18 Sequence 18, Appl
34 673 88.0 144 16 US-10-287-994-18 Sequence 18, Appl
35 673 88.0 144 16 US-10-659-295-27 Sequence 27, Appl
36 673 88.0 144 16 US-10-410-913-18 Sequence 18, Appl
37 673 88.0 144 16 US-10-666-123-3 Sequence 3, Appli
38 673 88.0 144 16 US-10-666-122-5 Sequence 5, Appli
39 673 88.0 144 17 US-10-901-417-15 Sequence 15, Appl
40 673 88.0 144 17 US-10-410-980-18 Sequence 18, Appl
41 673 88.0 191 15 US-10-449-831A-188 Sequence 188, App
42 673 88.0 610 9 US-09-783-708-1 Sequence 1, Appli
43 673 88.0 690 9 US-09-821-883-2 Sequence 2, Appli
44 671 87.7 127 16 US-10-658-834A-376 Sequence 376, App
45 670 87.6 127 16 US-10-658-834A-362 Sequence 362, App

ALIGNMENTS

RESULT 1

US-10-083-446-141
; Sequence 141, Application US/10083446
; Publication No. US20030185790A1

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olin, Peter O.
Paik, Kuman
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-10-083-446-141

Query Match 89.2%; Score 682; DB 14; Length 259;
Best Local Similarity 97.0%; Pred. No. 7.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 SGIEGRMAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQPT 68
DB 126 SGGGSNMAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQPT 185

QY 69 CLOTRLEYKQGLRSLTKLGPITMASHYKQHCPTPETSATQIITFESFKENLKDF 128
DB 186 CLOTRLEYKQGLRSLTKLGPITMASHYKQHCPTPETSATQIITFESFKENLKDF 245

QY 129 LLVIPDCWEPVQE 142
DB 246 LLVIPDCWEPVQE 259

RESULT 2
US-10-083-446-160
Sequence 160, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olin, Peter O.
Paik, Kuman
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-10-083-446-160

Query Match 88.6%; Score 678; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.5e-64;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQPTCLOTRL 74
DB 1 MAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQPTCLOTRL 60

QY 75 ELYKQGLRSLTKLGPITMASHYKQHCPTPETSATQIITFESFKENLKDFLLVIPF 134
DB 61 ELYKQGLRSLTKLGPITMASHYKQHCPTPETSATQIITFESFKENLKDFLLVIPF 120

QY 135 DCWEPVQE 142
DB 121 DCWEPVQE 128

RESULT 3
US-10-083-446-144
Sequence 144, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olin, Peter O.
Paik, Kuman
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-10-083-446-144

Query Match 88.6%; Score 678; DB 14; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 74
DB 147 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 206

QY 75 ELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFFLLVVPF 134
DB 207 ELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFFLLVVPF 266

QY 135 DCWEPVQE 142
DB 267 DCWEPVQE 274

RESULT 4
US-10-083-446-142
Sequence 142, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Ollins, Peter O.
Paik, Kuman
Thomas, John W.
TITLE OF INVENTION: Methods of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: S. Christopher Bauer, Pharmacia Corporation
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-083-446-142

Query Match 88.6%; Score 678; DB 14; Length 301;
Best Local Similarity 100.0%; Pred. No. 2.3e-63;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 74
DB 174 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAMNETVEVISEMFDLQETCLQTRL 233

QY 75 ELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFFLLVVPF 134
DB 234 ELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFFLLVVPF 293

QY 135 DCWEPVQE 142
DB 294 DCWEPVQE 301

RESULT 5
US-10-609-346-10
Sequence 10, Application US/10609346
Publication No. US20040063635A1
GENERAL INFORMATION:
APPLICANT: Yu, Zailin
APPLICANT: Fu, Yan
TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLO
TITLE OF INVENTION: EFFECTS
FILE REFERENCE: ZYU-0603
CURRENT APPLICATION NUMBER: US/10/609,346
CURRENT FILING DATE: 2003-06-26
PRIOR APPLICATION NUMBER: US 60/392,948
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 712
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HSA-GMCSF
US-10-609-346-10

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Query Match      88.2%; Score 675; DB 15; Length 712;
Best Local Similarity 99.2%; Pred. No. 1.5e-62;
Matches 127; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 74
Db 585 LAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 644

QY 75 ELYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 134
Db 645 ELYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 704

QY 135 DCWEPVQE 142
Db 705 DCWEPVQE 712

RESULT 6
US-09-821-883-18
; Sequence 18, Application US/09821883
; Patent No. US20020061310A1
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Laus, Reiner
; APPLICANT: Vidovic, Danir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; TITLE OF INVENTION: Cell-based Immunotherapy
; FILE REFERENCE: 7636-0022.30
; CURRENT APPLICATION NUMBER: US/09/821,883
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-883-18

Query Match      88.0%; Score 673; DB 9; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 75
Db 1 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 60

QY 76 LYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 135
Db 61 LYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127

RESULT 7
US-09-800-016-1
; Sequence 1, Application US/09800016
; Patent No. US20020141970A1
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; APPLICANT: Jochheim, Claudia
; TITLE OF INVENTION: STABLE AQUEOUS SOLUTIONS OF GRANULOCYTE MACROPHAGE COLONY-STIM
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 3253
; CURRENT APPLICATION NUMBER: US/09/800,016
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 127
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-016-1

Query Match      88.0%; Score 673; DB 9; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 75
Db 1 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 60

QY 76 LYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 135
Db 61 LYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127

RESULT 8
US-09-792-793A-15
; Sequence 15, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: GM-CSF
US-09-792-793A-15

Query Match      88.0%; Score 673; DB 9; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 75
Db 1 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLOEPTCLOTRL 60

QY 76 LYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 135
Db 61 LYKQGLRGSLLTKLKGPLTMASHYKQHCPTTSCATQIITFESFKENLKDFLLVIPF 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127

RESULT 9
US-10-400-377-8
; Sequence 8, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
```



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; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-8

Query Match      88.0%; Score 673; DB 14; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 75
Db 1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 135
Db 61 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127

RESULT 10
US-10-400-708-8
; Sequence 8, Application US/10400708
; Publication No. US2003016685A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-8

Query Match      88.0%; Score 673; DB 14; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 75
Db 1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 135
Db 61 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127

RESULT 11
US-10-298-148-8
; Sequence 8, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
```

```
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-8

Query Match      88.0%; Score 673; DB 14; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 75
Db 1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 135
Db 61 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127

RESULT 12
US-10-375-209A-15
; Sequence 15, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: GM-CSF
US-10-375-209A-15

Query Match      88.0%; Score 673; DB 15; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 75
Db 1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAENNETVEVISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 135
Db 61 LYKQGLRGSITKLKGLPLTMASHYKQHCPTPTSCATQIITPESPKENLKDFLLVIPFD 120

QY 136 CWEPVQE 142
Db 121 CWEPVQE 127
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RESULT 13
US-10-658-834A-202
; Sequence 202, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA98768
; DATABASE ENTRY DATE: 1996-05-02
US-10-658-834A-202

Query Match      88.0%; Score 673; DB 16; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDLQEPDCLQTRLE 75
DB 1 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFLLVIPFD 135
DB 61 LYKQGLRGSITKLGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFLLVIPFD 120

QY 136 CPEPVOE 142
DB 121 CPEPVOE 127

RESULT 14
US-10-743-295-5
; Sequence 5, Application US/10743295
; Publication No. US20040136952A1
; GENERAL INFORMATION:
; APPLICANT: Bhaskaran, Shyam S.
; APPLICANT: Sherman, Merry R.
; APPLICANT: Saifer, Mark G.P.
; APPLICANT: Williams, L. David
; TITLE OF INVENTION: POLYMER CONJUGATES OF CYTOKINES, CHEMOKINES, GROWTH FACTORS, POLY
; TITLE OF INVENTION: HORMONES AND ANTAGONISTS THEREOF WITH PRESERVED RECEPTOR-BINDING
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 2057.0060002/JAG/BJD
; CURRENT APPLICATION NUMBER: US/10/743,295
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 60/479,914
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: 60/436,020
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-743-295-5

Query Match      88.0%; Score 673; DB 16; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDLQEPDCLQTRLE 75
DB 1 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFLLVIPFD 135
DB 61 LYKQGLRGSITKLGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFLLVIPFD 120

QY 136 CPEPVOE 142
DB 121 CPEPVOE 127

RESULT 15
US-10-773-939-8
; Sequence 8, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,939
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-939-8

Query Match      88.0%; Score 673; DB 16; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-63;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDLQEPDCLQTRLE 75
DB 1 APARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDLQEPDCLQTRLE 60

QY 76 LYKQGLRGSITKLGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFLLVIPFD 135
DB 61 LYKQGLRGSITKLGPLTMASHYKQHCPTPTSCATQIITFESFKENLKDFLLVIPFD 120

QY 136 CPEPVOE 142
DB 121 CPEPVOE 127

Search completed: March 8, 2005, 16:26:00
Job time : 132 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 16:05:14 ; Search time 42 Seconds
(without alignments)
252.385 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHSSGIEGRMAPARS.....ENLKDFLLVPPDCWEPVQE 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	89.2	259	3 US-08-469-318-141	Sequence 141, App
2	682	89.2	259	3 US-08-468-609A-141	Sequence 141, App
3	682	89.2	259	3 US-08-446-872A-141	Sequence 141, App
4	682	89.2	259	4 US-08-762-227A-141	Sequence 141, App
5	682	89.2	259	5 PCT-US95-01185-141	Sequence 141, App
6	678	88.6	128	3 US-08-469-318-160	Sequence 160, App
7	678	88.6	128	3 US-08-468-609A-160	Sequence 160, App
8	678	88.6	128	3 US-08-446-872A-160	Sequence 160, App
9	678	88.6	128	4 US-08-762-227A-160	Sequence 160, App
10	678	88.6	128	5 PCT-US95-01185-160	Sequence 160, App
11	678	88.6	274	3 US-08-469-318-144	Sequence 144, App
12	678	88.6	274	3 US-08-468-609A-144	Sequence 144, App
13	678	88.6	274	3 US-08-446-872A-144	Sequence 144, App
14	678	88.6	274	4 US-08-762-227A-144	Sequence 144, App
15	678	88.6	274	5 PCT-US95-01185-144	Sequence 144, App
16	678	88.6	301	3 US-08-469-318-142	Sequence 142, App
17	678	88.6	301	3 US-08-468-609A-142	Sequence 142, App
18	678	88.6	301	3 US-08-446-872A-142	Sequence 142, App
19	678	88.6	301	4 US-08-762-227A-142	Sequence 142, App
20	678	88.6	301	5 PCT-US95-01185-142	Sequence 142, App
21	673	88.0	127	1 US-08-318-193-2	Sequence 2, Appli
22	673	88.0	127	4 US-09-462-941-8	Sequence 8, Appli
23	673	88.0	127	6 5229496-15	Patent No. 5229496
24	673	88.0	127	6 5229496-15	Patent No. 5229496
25	673	88.0	131	6 5229496-2	Patent No. 5229496
26	673	88.0	131	6 5229496-2	Patent No. 5229496
27	673	88.0	144	1 US-08-284-393B-11	Sequence 11, Appli

28 673 88.0 144 3 US-09-522-217-114 Sequence 114, App
29 673 88.0 144 4 US-09-923-246-114 Sequence 114, App
30 673 88.0 144 4 US-10-295-723-114 Sequence 114, App
31 673 88.0 144 5 PCT-US95-08950-11 Sequence 11, Appli
32 673 88.0 165 1 US-08-318-193-8 Sequence 8, Appli
33 673 88.0 168 1 US-08-318-193-10 Sequence 10, Appli
34 673 88.0 515 2 US-09-146-283-2 Sequence 2, Appli
35 673 88.0 515 3 US-08-579-823A-2 Sequence 2, Appli
36 673 88.0 515 3 US-09-344-195-2 Sequence 2, Appli
37 673 88.0 782 2 US-09-146-283-4 Sequence 4, Appli
38 673 88.0 782 3 US-08-579-823A-4 Sequence 4, Appli
39 673 88.0 782 3 US-09-344-195-4 Patent No. 5405952
40 669 87.5 127 6 5405952-2 Patent No. 5405952
41 669 87.5 127 1 US-08-225-224-4 Sequence 4, Appli
42 668 87.3 127 3 US-08-722-258-4 Sequence 4, Appli
43 668 87.3 127 5 PCT-US95-04468-4 Sequence 4, Appli
44 668 87.3 127 5 US-08-759-628-6 Sequence 6, Appli
45 668 87.3 144 3

ALIGNMENTS

RESULT 1
US-08-469-318-141
; Sequence 141, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 259 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-318-141

Query Match 89.2%; Score 682; DB 3; Length 259;
Best Local Similarity 97.0%; Pred. No. 1e-69;
Matches 130; Conservative 4; Mismatches 0; Gaps 0;
QY 9 SGIEGRMAPRSPSTQPEWHVNAIQEARRLLNSRDTAAENNETVEVISEMFDLQEPT 68
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Db 126 SGGSNMAIPRSPSTQPEWHVNAIQEARRLLNSRDTAAENNETVEVISEMFDLQEPT 185
QY 69 CLQTRLELYKQGLRGLSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLKDF 128
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Db 186 CLQTRLELYKQGLRGLSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLKDF 245
QY 129 LVVPPDCWEPVQE 142
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Db 246 LVVPPDCWEPVQE 259

RESULT 2
US-08-468-609A-141
; Sequence 141, Application US/08468609A

/ Patent No. 6030812
/ GENERAL INFORMATION:
/ APPLICANT: Abrams, Mark A.
/ APPLICANT: Bauer, S. C.
/ APPLICANT: Braford-Goldberg, Sarah R.
/ APPLICANT: Caparon, Mair H.
/ APPLICANT: Easton, Alan M.
/ APPLICANT: Klein, Barbara K.
/ APPLICANT: McKeane, John P.
/ APPLICANT: Olin, Peter O.
/ APPLICANT: Paik, Kuman
/ APPLICANT: Thomas, John W.
/ TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (II-3)
/ NUMBER OF SEQUENCES: 197
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
/ ADDRESSEE: Corporate Patent Dept.
/ STREET: P. O. Box 5110
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60680
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,609A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/192,325
/ FILING DATE: 14-FEB-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bennett, Dennis A.
/ REGISTRATION NUMBER: 34,547
/ REFERENCE/DOCKET NUMBER: C-2790/3
/ TELEPHONE: (314)737-6986
/ TELEFAX: (314)737-6972
/ INFORMATION FOR SEQ ID NO: 141:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 259 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-468-609A-141

Query Match 89.2%; Score 682; DB 3; Length 259;
Best Local Similarity 97.0%; Pred. No. 1e-69;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 SGIEGMAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDIQEPT 68
DB 126 SGGGNNAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDIQEPT 185

QY 69 CLOTRLELYKQGLRSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLKDF 128
DB 186 CLOTRLELYKQGLRSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLKDF 245

QY 129 LLVIPDCWEPVQE 142
DB 246 LLVIPDCWEPVQE 259

RESULT 3
US-08-446-872A-141
/ Sequence 141, Application US/08446872A
/ Patent No. 6361977
/ GENERAL INFORMATION:
/ APPLICANT: Abrams, Mark A.
/ Braford-Goldberg, Sarah R.

/ APPLICANT: Bauer, S. C.
/ APPLICANT: Braford-Goldberg, Sarah R.
/ APPLICANT: Caparon, Mair H.
/ APPLICANT: Easton, Alan M.
/ APPLICANT: Klein, Barbara K.
/ APPLICANT: McKeane, John P.
/ APPLICANT: Olin, Peter O.
/ APPLICANT: Paik, Kuman
/ APPLICANT: Thomas, John W.
/ TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
/ TITLE OF INVENTION: Fusion Protein
/ NUMBER OF SEQUENCES: 197
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
/ ADDRESSEE: Corporate Patent Dept.
/ STREET: P. O. Box 5110
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60680
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/446,872A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/192,325
/ FILING DATE: 14-FEB-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bennett, Dennis A.
/ REGISTRATION NUMBER: 34,547
/ REFERENCE/DOCKET NUMBER: C-2790/1
/ TELEPHONE: (314)737-6986
/ TELEFAX: (314)737-6972
/ INFORMATION FOR SEQ ID NO: 141:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 259 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-446-872A-141

Query Match 89.2%; Score 682; DB 3; Length 259;
Best Local Similarity 97.0%; Pred. No. 1e-69;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 SGIEGMAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDIQEPT 68
DB 126 SGGGNNAPARSPSTQPEWHVNAIQEARRLLNLSRDTAAENNETVEISEMFDIQEPT 185

QY 69 CLOTRLELYKQGLRSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLKDF 128
DB 186 CLOTRLELYKQGLRSLTKLKGPLTWASHYKQHCPTPTSCATQIITFESFKNLKDF 245

QY 129 LLVIPDCWEPVQE 142
DB 246 LLVIPDCWEPVQE 259

RESULT 4
US-08-762-227A-141
/ Sequence 141, Application US/08762227A
/ Patent No. 6436387
/ GENERAL INFORMATION:
/ APPLICANT: Abrams, Mark A.
/ Bauer, S. C.
/ Braford-Goldberg, Sarah R.

15	MAPARSPSPSTQPEHVHVAIQEARRLLNLSRDTAAENNETVEVISEMFDLOEPTCLOTRL	74
Qy		
1	MAPARSPSPSTQPEHVHVAIQEARRLLNLSRDTAAENNETVEVISEMFDLOEPTCLOTRL	60
Db		
75	ELYKQGLRGLSTLKGPLTMASHYKHQCPPTPETSCATQIIIFESPENKDKDFLLVDP	134
Qy		
61	ELYKQGLRGLSTLKGPLTMASHYKHQCPPTPETSCATQIIIFESPENKDKDFLLVDP	120
Db		
135	DCWEPVQOE	142
Qy		
121	DCWEPVQOE	128
Db		

RESULT 7
 US-08-468-609A-160
 ; Sequence 160, Application US/08468609A
 ; Patent No. 6030812
 ; GENERAL INFORMATION:
 ; APPLICANT: Abrams, Mark A.
 ; APPLICANT: Bauer, S. C.
 ; APPLICANT: Braford-Goldberg, Sarah R.
 ; APPLICANT: Caparon, Mairé H.
 ; APPLICANT: Easton, Alan M.
 ; APPLICANT: Klein, Barbara K.
 ; APPLICANT: McKeearn, John P.
 ; APPLICANT: Ollins, Peter O.
 ; APPLICANT: Paik, Kumman
 ; APPLICANT: Thomas, John W.
 ; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
 ; NUMBER OF SEQUENCES: 197
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 ; ADDRESSEE: Corporate Patent Dept.

[illegible]

RESULT 8
US-08-446-872A-160
; Sequence 160, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kumnun
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; TITLE OF INVENTION: Fusion Protein
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSES: Corporate Patent Dept.

	Query Match	88.6%;	Score 678;	DB 3;	Length 128;
	Best Local Similarity	100.0%;	Pred. No. 1.1e-69;		
	Matches 128;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	15	MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDAAEMNETVEVISEMFDIQEPTCLOTRL	74		
Db	1	MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDAAEMNETVEVISEMFDIQEPTCLOTRL	60		
QV	75	EIYKQGLRGLSLTKLKGPLTWASHYKHQCPPTPETSCATQIIIFSPFKENLKQPLLVIPF	134		

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/446,872
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 144:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 274 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-469-318-144

Query Match 88.6%; Score 678; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.2e-69;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISMFQLOBPTCLOTRL 74
DB 147 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISMFQLOBPTCLOTRL 206

QY 75 ELYKQGLRSLTKLKGPLTMASHYKQHCPPPTPETS CATQIITFESFKENLKDFLVIPP 134
DB 207 ELYKQGLRSLTKLKGPLTMASHYKQHCPPPTPETS CATQIITFESFKENLKDFLVIPP 266

QY 135 DCWEPVQE 142
DB 267 DCWEPVQE 274

RESULT 12
US-08-469-609A-144
; Sequence 144, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Ollins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972

;; INFORMATION FOR SEQ ID NO: 144:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 274 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-468-609A-144

Query Match 88.6%; Score 678; DB 3; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.2e-69;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISMFQLOBPTCLOTRL 74
DB 147 MAPARSPSPSTQPEWHVNAIQEARRLLNLSRDTAAEMNETVEVISMFQLOBPTCLOTRL 206

QY 75 ELYKQGLRSLTKLKGPLTMASHYKQHCPPPTPETS CATQIITFESFKENLKDFLVIPP 134
DB 207 ELYKQGLRSLTKLKGPLTMASHYKQHCPPPTPETS CATQIITFESFKENLKDFLVIPP 266

QY 135 DCWEPVQE 142
DB 267 DCWEPVQE 274

RESULT 13
US-08-446-872A-144
; Sequence 144, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Ollins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,872A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 144:
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; MOLECULE TYPE: protein
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; Sequence 144, Application US/08762227A
; Patent No. 6436387
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bratford-Goldberg, Sarah R.
; Caparon, Maire H.
; Easton, Alan M.
; Klein, Barbara K.
; Mckearn, John P.
; Olin, Peter O.
; Paik, Kumnan
; Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; FUSION PROTEIN
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
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; FILING DATE: 09-Dec-1996
; CLASSIFICATION: <Unknown>
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; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
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; Sequence 144, Application PC/TUS9501185
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; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
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; FILING DATE: 02-FEB-1995
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	318.4	69.5	392	6	I49837	I49837 Sequence 1
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ALIGNMENTS

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DEFINITION BamHI-HindIII fragment in vector pAEO.GMCSF.
ACCESSION A20088
VERSION A20088.1 GI:583268
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 905)
AUTHORS Garvin,R.T. and Malek,L.T.
TITLE An expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomyces
JOURNAL Patent: EP 0352707-A 21 31-JAN-1990;
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DEFINITION BamHI-HindIII fragment in vector pABO.GMCSF.
ACCESSION A20089
VERSION 1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM Garvin,R.T. and Malek,L.T.
REFERENCE 1 (bases 1 to 906)
AUTHORS Garvin,R.T. and Malek,L.T.
TITLE An expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomycetes
JOURNAL Patent: EP 0352707-A 22 31-JAN-1990;
Cangene Corporation
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Db 348 AGCAGTGAACGGATCCAGAGGCGCGAGGCTCTCAACCTCTCGGCGACACCGCG 289

Qy 155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCCGATCTCCAGGAGCCGACCT 214

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Db 108 COTGTGGCCACCCAGATCATCAGTTCGAGTCTTCAAGGAGAACTCAAGGACTTCC 49

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Db 562 AGCAGTGAACGGATCCAGAGGCGCGAGGCTCTCAACCTCTCGGCGACCGCG 621

Qy 155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCCGATCTCCAGGAGCCGACCT 214

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Db 682 GCCTCCAGACCCCGCTCGAGCTGTACAAGCAGGCGCTCCGGCGAGCCTCAACAGCTCA 741

Qy 275 AGGGCCCGCTACCATGATGGGTCCCACTCAAGCAGCAGTGGCCACCGACCGCGAGA 334

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Qy 335 CCTCTCGGCGCACCCAGATCATCCTTCGAGGCTTCAAGGAGAACTCAAGGACTTCC 394

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RESULT 5
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LOCUS      384 bp DNA linear PAT 18-AUG-1994
DEFINITION Peti-Hind III fragment encoding GM-CSF.
ACCESSION A20082
VERSION A20082.1 GI:583266
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 384)
AUTHORS   Garvin,R.T. and Malek,L.T.
TITLE     An expression system for the secretion of bioactive human
          granulocyte macrophage colony stimulating factor (GM-CSF) and other
          heterologous proteins from streptomyces
JOURNAL    Patent: EP 0352707-A 13 31-JAN-1990;
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DB 328 GAGGCGCGCGCTCTCAACCTCTCGCGGACACCGCGCGGAGTGAACGAGACCGTG 269
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DB 268 GAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAG 209
QY 235 CTGTACAAGCAGGCGCTCCGCGGAGCTTCACCAAGCTCAAGGGCCGCTCACCATGATG 294
DB 208 CTGTACAAGCAGGCGCTCCGCGGAGCTTCACCAAGCTCAAGGGCGCTGACCATGATG 149
QY 295 GGTCTCCACTACAGGAGCACTGCCACCGACCCCGGAGACCTCTCTGCGCCACCCAGATC 354
DB 148 GGTCTCCACTACAAACAGCACTGCCCCCGACCGCGGAGACGTCGTCGCGCCACCCAGATC 89
QY 355 ATCACCTTCGAGGCTTCAAGGAGAACCTCAAGGACTTCTCTCTCGTGTATCCGTTTCGAC 414
DB 88 ATCACCTTCGAGTCTGTTCAAGGAGAACCTCAAGGACTTCTCTCTCGTGTATCCGTTTCGAC 29
QY 415 TGCTGGAGCCGCTGCAGGAGTGA 438

RESULT 6
A20083/c
LOCUS      392 bp DNA linear PAT 18-AUG-1994
DEFINITION Peti-Hind III fragment encoding GM-CSF.
ACCESSION A20083
VERSION A20083.1 GI:578981
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 392)
AUTHORS   Garvin,R.T. and Malek,L.T.
TITLE     An expression system for the secretion of bioactive human
          granulocyte macrophage colony stimulating factor (GM-CSF) and other
          heterologous proteins from streptomyces
JOURNAL    Patent: EP 0352707-A 14 31-JAN-1990;
          Cangene Corporation
FEATURES   Location/Qualifiers
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              /db_xref="taxon:32630"

ORIGIN

Query Match      69.5%; Score 318.4; DB 6; Length 392;
Best Local Similarity 89.3%; Pred. No. 5.6e-38;
Matches 343; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 55 GCGCCAGCGCGAGCGCCGCTCCACCCAGCGCTGGAGCAGCTGTAACGCGATCCAG 114
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DB 328 GAGGCGCGCGCTCTCAACCTCTCGCGGACACCGCGCGGAGTGAACGAGACCGTG 269
QY 175 GAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAG 234
DB 268 GAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAG 209
QY 235 CTGTACAAGCAGGCGCTCCGCGGAGCTTCACCAAGCTCAAGGGCCGCTCACCATGATG 294
DB 208 CTGTACAAGCAGGCGCTCCGCGGAGCTTCACCAAGCTCAAGGGCGCTGACCATGATG 149
QY 295 GGTCTCCACTACAGGAGCACTGCCACCGACCCCGGAGACCTCTCTGCGCCACCCAGATC 354
DB 148 GGTCTCCACTACAAACAGCACTGCCCCCGACCGCGGAGACGTCGTCGCGCCACCCAGATC 89
QY 355 ATCACCTTCGAGGCTTCAAGGAGAACCTCAAGGACTTCTCTCTCGTGTATCCGTTTCGAC 414
DB 88 ATCACCTTCGAGTCTGTTCAAGGAGAACCTCAAGGACTTCTCTCTCGTGTATCCGTTTCGAC 29
QY 415 TGCTGGAGCCGCTGCAGGAGTGA 438
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235 C T G T A C A A G C A G G C C T C C G C G C A G C C T C A C A A G C T C A A G G C C C G C T C A C C A T G A T G 294
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88 A T C A C G T T C A G T C G T T C A A G G A G A A C C T G A A G A C T T C C T C C T G A T C C C C T T C G A C 29
415 T G C T G G A G C C G T G C A G G A T G A 438
28 T G C T G G A G C C G T G C A G G A T G A 5

RESULT 10
LOCUS AR363244 896 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 2 from patent US 5200327.
ACCESSION AR363244
VERSION AR363244.1 GI:34424297
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 896)
AUTHORS Garvin, R.T. and Malek, L.T.
TITLE Expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomycetes
JOURNAL Patent: US 5200327-A 2 06-APR-1993;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Query Match 69.5%; Score 318.4; DB 6; Length 896;
Best Local Similarity 89.3%; Pred. No. 4.7e-38;
Matches 343; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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115 G A G G C C C G C A G G T C C T C A A C C T C T C C C G C G A C A C C C G C C G A G A T G A A C G A C C G T G 174
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633 G A G G T G A T C T C G A G A T G T T C G A C T T G C A G A G C C C A C G T G C C T C C A G A C C C G C C T C G A G 692
235 C T G T A C A A G C A G G C C T C C G C G C A G C C T C A C A A G C T C A A G G C C C G C T C A C C A T G A T G 294
693 C T G T A C A A G C A G G C C T C C G C G C A G C C T C A C A A G C T C A A G G C C C G C T G A C C A T G A T G 752
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415 T G C T G G A G C C C G T G C A G G A T G A 438
873 T G C T G G A G C C C G T G C A G G A T G A 896

RESULT 12
LOCUS AR363243 386 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5200327.
ACCESSION AR363243
VERSION AR363243.1 GI:34424296
KEYWORDS
SOURCE
ORGANISM

355 A T C A C C T T C G A G A C T T C A A G G A G A A C C T C A A G G A C T T C C T C C T G A T C C G G T T C G A C 414
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415 T G C T G G A G C C C G T G C A G G A T G A 438
873 T G C T G G A G C C C G T G C A G G A T G A 896

RESULT 11
LOCUS I49838 900 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5641663.
ACCESSION I49838
VERSION I49838.1 GI:2472058
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 900)
AUTHORS Garvin, R.T. and Malek, L.T.
TITLE Expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomycetes
JOURNAL Patent: US 5641663-A 7 24-JUN-1997;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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Query Match 69.5%; Score 318.4; DB 6; Length 900;
Best Local Similarity 89.3%; Pred. No. 4.7e-38;
Matches 343; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
55 G C G C C A G C G C G C A G C C C G C G T C C A C C C A G C C G T G G G A G C A C G T G A A C G C G A T C C A G 114
513 G C C C C G C C G C G T C G C C T C G C C G T C G A C C C A G C C G T G G G A G C A C G T C A A C G C G A T C C A G 572
115 G A G G C C C G C A G G T C C T C A A C C T C T C C C G C G A C A C C C G C C G A G A T G A A C G A C C G T G 174
573 G A G G C C C G C G C T G T C A A C C T C T C G C G G A C A C G C C C G C G A G A T G A A C G A C C G T G 632
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633 G A G G T G A T C T C G A G A T G T T C G A C T T G C A G A G C C C A C G T G C C T C C A G A C C C G C C T C G A G 692
235 C T G T A C A A G C A G G C C T C C G C G C A G C C T C A C A A G C T C A A G G C C C G C T C A C C A T G A T G 294
693 C T G T A C A A G C A G G C C T C C G C G C A G C C T C A C A A G C T C A A G G C C C G C T G A C C A T G A T G 752
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813 A T C A C G T T C G A G T C G T T C A A G G A G A A C C T G A A G G A C T T C C T C C T G A T C C C C T T C G A C 872
415 T G C T G G A G C C C G T G C A G G A T G A 438
873 T G C T G G A G C C C G T G C A G G A T G A 896

RESULT 12
LOCUS AR363243 386 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5200327.
ACCESSION AR363243
VERSION AR363243.1 GI:34424296
KEYWORDS
SOURCE
ORGANISM

Unclassified.	
REFERENCE	1 (bases 1 to 386)
AUTHORS	Garvin,R.T. and Malek,L.T.
TITLE	Expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomyces
JOURNAL	Patent: US 5200327-A 1 06-APR-1993;
FEATURES	Location/Qualifiers
source	1..386
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QY	76 CCGTCCACCCAGCGCTGGGAGACGTGAACGGGATCCAGGAGCCCGCAGGCTCTCAAC 135
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Db	84 CTCTCCGGGACACCGCCCGGAGATGAACGAGACCGTGGAGTGATCTCGGAGATGTTTC 143
QY	196 GATCTCCAGGAGCCGACCTGCTCTCCAGACCCCGCTCGAGCTGTACAAAGCAGGCGCTCCGC 255
Db	144 GACTTCAGGAGCCACGCTGCTCTCCAGACCCCGCTCGAGCTGTACAAAGCAGGCGCTCCGG 203
QY	256 GGCAGCTCACCAAGCTCAAGGGCCCGCTCAACATGATGGTCCCACTACAAAGCAGCAC 315
Db	204 GGCAGCTCACCAAGCTCAAGGGCCCGCTGACCATGATGGCGTCCCACTACAAAGCAGCAC 263
QY	316 TGCCCAACGACCCCGGAGACCTCTCGGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAG 375
Db	264 TGCCCCCAGCAGCGGAGAGCTGTGCGGCCACCCAGATCATCACCTTCGAGTGTTCAG 323
QY	376 GAGAACTCAAGGACTTCTCTCTGTGATCCCGTTCGACTGTGGAGCGGTGCAGGAG 435
Db	324 GAGAACTCAAGGACTTCTCTCTGTGATCCCGTTCGACTGTGGAGCGGTGCAGGAG 383
QY	436 TGA 438
Db	384 TGA 386
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LOCUS	CQ834915 435 bp DNA linear PAT 29-JUL-2004
DEFINITION	Sequence 2 from Patent WO2004059556.
ACCESSION	CQ834915
VERSION	CQ834915.1 GI:50834452
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Raab,D., Graf,M., Norka,F. and Wagner,R.
JOURNAL	Method and device for optimizing a nucleotide sequence for the purpose of expression of a protein
FEATURES	Patent: WO 2004059556-A 2 15-JUL-2004;
source	Geneart GmbH (DE)
Location/Qualifiers	
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Matches 321; Conservative	0; Mismatches 61; Indels 0; Gaps 0;
QY	55 GCGCCAGCGCGAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACCGCATCCAG 114
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QY	115 GAGGCCCGAGGCTCTCTCAACTCTCCCGGAGCACCGCGCGCGGAGATGAACAGACCGTGG 174
Db	112 GAGGCCCGAGGACTCTCTGAACCTGAGCAGAGATACAGCGCGCGGAGATGAACAGACCGTGG 171
QY	175 GAGGTGATCTCCGAGATGTTGATCTCCAGGAGCGGACCTGCCTCCAGACCGCGCTCGAG 234
Db	172 GAGGTGATCAGCGAGATGTTGACCTGCAGGAGCCTCATGCTCGAGACCGCGGTGGAG 231
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QY	295 GCGTCCCACTACAAGCAGACGTGCCCAACGAGCCCGGAGACCTCTCTGGCGCACCCAGATC 354
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QY	355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCTCTCTGTGATCCCGTTCGAC 414
Db	352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCTCTGTGATCCCGTTCGAT 411
QY	415 TGCTGGGAGCCCGTGCAGGAGT 436
Db	412 TGCTGGGAGCCCGTGCAGGAGT 433
RESULT 14	
LOCUS	AR202206 777 bp DNA linear PAT 20-APR-2002
DEFINITION	Sequence 55 from patent US 6361977.
ACCESSION	AR202206
VERSION	AR202206.1 GI:20256745
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 777)
AUTHORS	Bauer, S.Christopher., Abrams,M.Allen., Braford-Goldberg, S.Ruth., Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.P., Olin, P.O., Paik, K. and Thomas, J.W.
TITLE	Methods of using multivariant IL-3 hematopoiesis fusion protein
JOURNAL	Patent: US 6361977-A 55 26-MAR-2002;
FEATURES	Location/Qualifiers
source	1..777
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/mol_type="unassigned DNA"	
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Query Match	61.9%; Score 283.6; DB 6; Length 777;
Best Local Similarity	81.6%; Pred. No. 7.1e-33;
Matches 328; Conservative	0; Mismatches 74; Indels 0; Gaps 0;
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QY	94 GAGCAGTGAACGCGATCCAGGAGCGCGCGAGGCTCTCAACTCTCCCGCGACACCGCC 153
Db	436 GAAACGTTGAATGCCATCCAGGAGCGCGGCTCTCTCTGAACTCTAGTAGACACTGTCT 495
QY	154 GCCGAGATGAACGAGACCGTGGAGTGATCTCCGAGATGTTGATCTCCAGGAGCGGACC 213
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QY	214 TGCCTCCAGACCCCGCTCGAGCTGTACAGCAGGCGCTCCCGCGGAGCGCTCAACAGTTC 273
Db	556 TGCCTACAGACCCCGCTCGAGCTGTACAGCAGGCGCTCCCGGGCAGCGCTCACCAGCTC 615
QY	274 AAGGGCGCGCTCACCATGATGCGGTCCCACTACAAGAGCAGCTGCCACCCGACCCCGGAG 333

Db 616 AAGGGCCCTTGACCATGATGGCCAGCCACTACAGCAGCACTGCCCTCCAAACCCCGGAA 675
Qy 334 ACCTCTGCGCCACCCAGATCATCCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
Db 676 ACTTCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735
Qy 394 CTCCTCGTGATCCGGTTCGACTGCTGGAGCCGGTGCAGGAG 435
Db 736 CTGCTTGTATCCCTTTGACTGCTGGAGCCAGTCCAGGAG 777

RESULT 15

AR223208
LOCUS AR223208 777 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 55 from patent US 6436387.
ACCESSION AR223208
VERSION AR223208.1 GI:233331216

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 777)

AUTHORS
Bauer, S.C., Abrams, M.A., Braford-Goldberg, S.P., Caparon, M.H.,
Easton, A.M., Klein, B.K., McKeam, J.P., Olin, P.O., Paik, K. and
Thomas, J.W.

TITLE
Methods of ex-vivo expansion of hematopoietic cells using

JOURNAL
multivariant IL-3 hematopoiesis chimera proteins

FEATURES
Patent: US 6436387-A 55 20-AUG-2002;

Location/Qualifiers

source 1..777

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 61.9%; Score 283.6; DB 6; Length 777;
Best Local Similarity 81.8%; Pred. No. 7.1e-33;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
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Qy 154 GCGGAGTGAACGAGCCGTGGAGGTGATCTCCGAGATGTTGATCTCCAGGAGCCGACC 213
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Db 736 CTGCTTGTATCCCTTTGACTGCTGGAGCCAGTCCAGGAG 777

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OM nucleic - nucleic search, using sw model

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Title: US-10-723-083-1

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	318.4	69.5	392	1	US-08-318-193-1
5	318.4	69.5	896	6	5200327-2
6	318.4	69.5	896	6	5200327-2
7	318.4	69.5	900	1	US-08-318-193-7
8	315	68.8	386	6	5200327-1
9	315	68.8	386	6	5200327-1
10	312.6	68.3	435	4	US-10-188-056-31
11	311	67.9	435	4	US-10-188-056-33
12	283.6	61.9	777	3	US-08-469-318-55
13	283.6	61.9	777	3	US-08-468-609A-55
14	283.6	61.9	777	3	US-08-446-872A-55
15	283.6	61.9	777	3	US-08-762-227A-55
16	283.6	61.9	777	3	PCT-US95-01185-55
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19	283	61.8	402	3	US-08-446-872A-176
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21	283	61.8	402	5	PCT-US95-01185-176
22	281	61.4	822	3	US-08-469-318-69
23	281	61.4	822	3	US-08-468-609A-69
24	281	61.4	822	3	US-08-446-872A-69
25	281	61.4	822	3	US-08-762-227A-69
26	281	61.4	822	5	PCT-US95-01185-69
27	281	61.4	903	3	US-08-469-318-66

28	281	61.4	903	3	US-08-468-609A-66	Sequence 66, Appl
29	281	61.4	903	3	US-08-446-872A-66	Sequence 66, Appl
30	281	61.4	903	3	US-08-762-227A-66	Sequence 66, Appl
31	281	61.4	903	5	PCT-US95-01185-66	Sequence 3, Appl
32	276.8	60.4	2385	2	US-09-146-283-3	Sequence 3, Appl
33	276.8	60.4	2385	3	US-08-579-823A-3	Sequence 3, Appl
34	276.8	60.4	2385	3	US-09-344-195-3	Sequence 3, Appl
35	276.2	60.3	660	6	5391485-2	Patent No. 5391485
36	276.2	60.3	660	6	5391485-2	Patent No. 5391485
37	276.2	60.3	661	6	5229496-1	Patent No. 5229496
38	276.2	60.3	661	6	5229496-1	Patent No. 5229496
39	276.2	60.3	1011	4	US-09-976-594-275	Sequence 275, App
40	275.8	60.2	435	3	US-08-848-760B-8	Sequence 8, Appl
41	275.8	60.2	435	4	US-09-826-025-8	Sequence 8, Appl
42	275.2	60.1	756	4	US-09-016-434-1195	Sequence 1195, Ap
43	275.2	60.1	1318	3	US-09-310-842-3	Sequence 3, Appl
44	274.6	60.0	1011	2	US-08-750-128-12	Sequence 12, Appl
45	274.6	60.0	1588	2	US-09-146-283-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
5200327-3
; Patent No. 5200327
; APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
; BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
; FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/224,568
; FILING DATE: 26-JUL-1988
; SEQ ID NO:3
; LENGTH: 905
5200327-3

Query Match 69.7%; Score 319.2; DB 6; Length 905;
Best Local Similarity 86.9%; Pred. No. 1e-60;
Matches 351; Conservative: 0; Mismatches 53; Indels 0; Gaps 0;

QY	35	CGGGCATCGAGGGCGCGATGCGCGCAGCGCGCGAGCGCGCGTCCACCGAGCCGCTCCACCGAGCCGCTGGG	94
DB	502	CGGCTCCGGGGCGTGTGCGAGCCCGCGCGCGCTCGCCCTCGCGCTCGAGCCCGCTGGG	561
QY	95	AGCAGTGAACGGGATCCAGAGGGCGCGAGGCTCTCAACCTCTCCCGGACACCGCG	154
DB	562	AGCAGTGAACGGGATCCAGAGGGCGCGCGCTCTCAACCTCTCGCGGACACCGCG	621
QY	155	CGGAGATGAACGAGACCGGTGGAGGTGATCTCGAGATGTTTCGATCTCCAGGAGCGACCT	214
DB	622	CGGAGATGAACGAGACCGGTGGAGGTGATCTCGAGATGTTTCGATCTCCAGGAGCGACCT	681
QY	215	GCCTCCAGACCGCGCTCGAGCTGTATCAAGCAGGGCTCCCGGCGACCTCCACCAAGCTCA	274
DB	682	GCCTCCAGACCGCGCTCGAGCTGTATCAAGCAGGGCTCCCGGCGACCTCCACCAAGCTCA	741
QY	275	AGGGCGGCTCACCATGATGGCGTCCCACTACAGCAGCACTGCCCGACCGGAGGAGG	334
DB	742	AGGGCGGCTCACCATGATGGCGTCCCACTACAAACAGCAGCACTGCCCGGAGGAGG	801
QY	335	CTCTCTGCGCCACCGAGATCATCCTTCGAGAGCTTCAAGGAGAGCACTCAAGGACTTCC	394
DB	802	CTCTCTGCGCCACCGAGATCATCCTTCGAGAGCTTCAAGGAGAGCACTCAAGGACTTCC	861
QY	395	TCCTCTGATCGGCTTCGAGCTGCGGAGCGCGTGCAGGAGTGA	438
DB	862	TCCTCTGATCGGCTTCGAGCTGCGGAGCGCGTGCAGGAGTGA	905

RESULT 2


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RESULT 6
5200327-2
; Patent No. 5200327
; APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
; BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
; FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/224,568
; FILING DATE: 26-JUL-1988
; SEQ ID NO:2
; LENGTH: 896
5200327-2

Query Match 69.5%; Score 318.4; DB 6; Length 896;
Best Local Similarity 89.3%; Pred. No. 1.5e-60;
Matches 343; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 55 GCSCGACGGCGCAGCCGAGCCCGTCACCCAGCCGTGGGAGACACGTGAACGCCATCCAG 114
Db 513 GCCCCGCGCCGGTCGCGCTCGCCGTGACCCAGCCGTGGGAGACACGTCAACGCCATCCAG 572

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Db 204 GGCAGCCTCACCAGCTCAAGGGCGCTGACCATGATGGCTCCCACTACAAACAGCAC 263
QY 316 TGCCACCGACCCCGGAGACTCTCTGGCCACCCAGATCATCACTTTCGAGAGCTTCAAG 375
Db 264 TGCCCCCCCCAGCGCGGAGAGCTGCTGGCCACCCAGATCATCACTTTCGAGTGTTCAG 323
QY 376 GAGAACTCAAGAGACTTCTCTCTGATCCCGTTCGACTGCTGGGAGCGGTTCAGGAG 435
Db 324 GAGAACTGAAGAGACTTCTCTCTGATCCCTTCGACTGCTGGGAGCGGTTCAGGAG 383
QY 436 TGA 438
Db 384 TGA 386

RESULT 9
US-10-188-056-31
; Patent No. 5200327
; APPLICANT: GARVIN, ROBERT T.; MALEK, LAWRENCE T.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
; BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
; FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/224,568
; FILING DATE: 26-JUL-1998
; SEQ ID NO: 1:
; LENGTH: 386
5200327-1

Query Match 68.8%; Score 315; DB 6; Length 386;
Best Local Similarity 91.7%; Pred. No. 7.5e-60;
Matches 333; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 76 CGCTCACCAGCGCTGGGAGCAGCTGAAGCGCATCCAGAGGCGCGCAGGCTCTCAAC 135
Db 24 CGCTCACCAGCGCTGGGAGCAGCTGAAGCGCATCCAGAGGCGCGCAGGCTCTCAAC 83
QY 136 CTCTCCCGGACACCGCGCGGAGATGAACGAGACCGTGGAGTGATCTCCGAGATGTTTC 195
Db 84 CTCTCCCGGACACCGCGCGGAGATGAACGAGACCGTGGAGTGATCTCCGAGATGTTTC 143
QY 196 GATCTCCAGAGCGCAGCTCTCTCCAGACCGCGCTCGAGCTGTACAAGCAGGCGCTCCGC 255
Db 144 GACTTCAGAGGCGCAGCTCTCTCCAGACCGCGCTCGAGCTGTACAAGCAGGCGCTCCGC 203
QY 256 GGCAGCCTCACCAGCTCAAGGCGCGCTCACCATGATGGCGTCCCACTACAGAGCAGC 315
Db 204 GGCAGCCTCACCAGCTCAAGGCGCGCTGACCATGATGGCGTCCCACTACAAACAGCAC 263
QY 316 TGCCACCGACCCCGGAGACTCTCTGGCCACCCAGATCATCACTTTCGAGAGCTTCAAG 375
Db 264 TGCCCCCCCCAGCGCGGAGAGCTGCTGGCCACCCAGATCATCACTTTCGAGTGTTCAG 323
QY 376 GAGAACTCAAGAGACTTCTCTCTGATCCCGTTCGACTGCTGGGAGCGGTTCAGGAG 435
Db 324 GAGAACTGAAGAGACTTCTCTCTGATCCCTTCGACTGCTGGGAGCGGTTCAGGAG 383
QY 436 TGA 438
Db 384 TGA 386

RESULT 10
US-10-188-056-31
; Sequence 31, Application US/10188056
; Patent No. 6809191
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.

; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188,056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-31

Query Match 68.3%; Score 312.6; DB 4; Length 435;
Best Local Similarity 82.8%; Pred. No. 2.6e-59;
Matches 357; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 8 GGATGCACCAACCAACCACTCTCTCGGCATCGAGGGCGCATGGGCCAGCGCGCA 67
Db 5 GGCTGCAGAGCTGTCTCTGTGGGCACCGTGGCCCTGCAGCATCAGCGTCCCGCCAGAA 64
QY 68 GCCGAGCCCGTCCACCCAGCCGCTGGGAGCACGCTGAACGCGATCCAGAGGCGCCGAGGC 127
Db 65 GCCCAGCCCTCCACCCAGCCCTGGGAGCACGCTGAACGCGATCCAGAGGCGCCAGAGGC 124
QY 128 TCCTCAACCTCTCCCGGACACCGCCCGGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
Db 125 TGCTGAACCTGTCCAGAGACACCGCCCGGAGATGAACGAGACCGTGGAGGTGATCAGCG 184
QY 188 AGATGTTTCGATCTCCAGAGCGCGACCTGCTCCAGACCGCCCTCGAGCTGTACAAGCAGG 247
Db 185 AGATGTTTCGATCTCCAGAGCGCGACCTGCTCCAGACCGCCCTCGAGCTGTACAAGCAGG 244
QY 248 GCCTCCGCGGCGCTCTCACAAGCTCAAGGGCGCGCTCACCATGATGGCGTCCCACTACA 307
Db 245 GACTCGGGGCGAGCTGACCAAGCTGAAGGAGCCCTTGACCATGATGGCCAGCCACTACA 304
QY 308 AGCAGACTTGCCACCGACCGCCGAGACCTCTTGCGCCACCCAGATCATCACTTTCGAGA 367
Db 305 AGCAGACTTGCCCTCTCCACACCGCAGACGAGCTGCGCCACCCAGATCATCACTTTCGAGA 364
QY 368 GCTTCAAGAGAGACCTCAAGGACTTCTCTCTGATCCCGTTCGACTGCTGGAGCGCG 427
Db 365 GCTTCAAGAGAGACCTTGAAGGACTTCTCTCTGATCCCTCTGATCCCTCTGAGGCGCG 424
QY 428 TGCAGGAGTGA 438
Db 425 TGCAGGAGTGA 435

RESULT 11
US-10-188-056-33
; Sequence 33, Application US/10188056
; Patent No. 6809191
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188,056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-33

Query Match 67.9%; Score 311; DB 4; Length 435;
Best Local Similarity 82.6%; Pred. No. 5.7e-59;
Matches 356; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 8 GGATGACACCAACCAACCACTCTCTCGGCATCGAGGGCCGCAATGGCGCCAGCGCGCA 67
DB 5 GGCTGCAGAGCGTGTCTCTGCTGGGCACCGTGGCCCTGCAGCATCAGCGCTCCCGCCAGAA 64
QY 68 GCCGAGCCCGTCCACCGAGCCGTGGGAGCAGTGAACCGGATCCAGGAGCCCGCAGGC 127
DB 65 GCCCCAGCCCTCCACCCAGCCCTGGGAGCAGTGAACCGGATCCAGGAGCCCGCAGGC 124
QY 128 TCTCAACCTCTCCCGCAGCACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
DB 125 TGTGNACTGTTCAGAGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCAGGC 184
QY 188 AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTTCGAGCTGTTCAGAGCG 247
DB 185 AGATGTTGACCTGCAGGAGCCACCTGCTTCGAGACCCGCTTCGAGCTGTTCAGAGCG 244
QY 248 GCTCCGCGGAGCCTCACAAGCTCAAGGCGCCGCTCAACGATGAGGCGTCCACTACA 307
DB 245 GACTCGGGGCGACCTGACCAAGCTGAAGGAGCCCGCTGACCATGATGGCCAGCCACTACA 304
QY 308 AGCAGACTGCCACCGACCGGAGACCTCTCTGCGCCACCCAGATCATCACTTCGAGA 367
DB 305 AGCAGACTGCCCTCCACACCGGAGACGAGCTGCGCCACCCAGACCATCACTTCGAGA 364
QY 368 GCTTCAAGGAGAACTCAAGGACTTCTCTCTGATCCCGTTCGATCCCGTTCGAGCGCG 427
DB 365 GCTTCAAGGAGAACTGAAGGACTTCTCTGATCCCGTTCGATCCCGTTCGAGCGCG 424
QY 428 TGCAGGAGTGA 438
DB 425 TGCAGGAGTGA 435

RESULT 12
US-08-469-318-55
; Sequence 55, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-318-55
Query Match 51.9%; Score 283.6; DB 3; Length 777;
Best Local Similarity 81.8%; Pred. No. 5.8e-53;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 34 TCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 93
DB 376 TCTGGCGGCGGCTCCACATGCGGCGGCTGCTTCCCGGCTCCCGCTACCCAGCGCGTGG 435
QY 94 GAGCAGTGAAACGCGATCCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 153

DB 436 GAACACGTGAATGCCATCCAGGAGCCCGCGCTCTCTGAACCTGAGTAGACACTGCT 495
QY 154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCTCCGAGATGTTCCGATCTCCAGGAGCCGACC 213
DB 496 GCTGAGATGAATGAACAGTAGAAGTATATCAGAAATGTTTGACCTCCAGGAGCGGACT 555
QY 214 TGCCTCCAGACCCGCTCGAGCTGTACAGAGGCGCTCCGCGGAGCCTTCAAGGACTTC 273
DB 556 TGCCTACAGACCCGCTCGAGCTGTACAGAGGCGCTCCGCGGAGCCTTCAAGGACTTC 615
QY 274 RAGGCGCCGCTCACCATGATGCGTCCCACTACAGAGCAGCTGCCACCGACCCGCGAG 333
DB 616 AAGGCGCCCTTGACCATGATGCGGAGCCACTACAGAGCAGCTGCCCTCAACCCCGGAA 675
QY 334 ACCTCTCGCGCCACCCAGATCATCACTTCGAGAGCTTCAAGGAGAACTCAAGGACTTC 393
DB 676 ACTTCTGTGCAACCCAGATTCACCTTTGAAAGTTTCAAGAGAGAACCTGAAGGACTTC 735
QY 394 CTCCTCGTATCCCGTTCGACTGCTGGGAGCGGCTGCAGGAG 435
DB 736 CTGCTTGTATCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 13
US-08-468-609A-55
; Sequence 55, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-3)
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-446-872A-55

Query Match 61.9%; Score 283.6; DB 3; Length 777;
Best Local Similarity 81.6%; Pred. No. 5.8e-53;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0

QY 34 TCCGGCATCGAGGGCCGCGATGGCGCCAGCGCGAGCCGCGAGCCGCGTCCACCCAGCCGTTGG 93
DB 376 TCTGGCGCGCGCTCCCAACATGGCACCGGCTCGTTCCCGCTCCCGCTTACCCAGCCGTTGG 435
QY 94 GAGCAGCTGAACCGCATGCAGGAGGGCCGCGAGGCTCTCTCAACCTCTCCCGCGACACCGCC 153
DB 436 GAACAGCTGATGCCATCCAGGAGGGCCGCGCTCTCTGAACCTGAGTAGAGACACTGCT 495
QY 154 GCCGAGATGAACGAGACCGCTGGAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCCGACC 213
DB 496 GCTGAGATGAATGAACACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555
QY 214 TGCCTCAGACCCGCTCGAGCTGTACAGCAGGGGCTCCGCGGAGCCTTCAAGGAGTTC 273
DB 556 TGCCTACAGACCCGCTCGAGCTGTACAGCAGGGGCTTCGCGGAGCAGCTTCAAGGAGTTC 615
QY 274 AAGGGCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAGTCCCAACCGACCCCGGAG 333
DB 616 AAGGGCCCTTGACCATGATGGCAGGCACCTACAGCAGCAGTCTGCCCTTCAAGGAGTTC 675
QY 334 ACCTCTCGGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGAGTTC 393
DB 676 ACTTCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAGGAGAACCTCAAGGAGTTC 735
QY 394 CTCCTCGTATCCGTTGACTGCTGGAGCCCGTGGAGGAG 435
DB 736 CTGCTTGTATCCCTTTGACTGCTGGAGGCCAGTCCAGGAG 777

RESULT 15
US-08-762-227A-55
Sequence 55, Application US/08762227A
Patent No. 6436387
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maïre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110

/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60680
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/762,227A
/ FILING DATE: 09-Dec-1996
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/192,325
/ FILING DATE: 14-FEB-1994
/ APPLICATION NUMBER: US 08/446,872
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bennett, Dennis A.
/ REGISTRATION NUMBER: 34,547
/ REFERENCE/DOCKET NUMBER: C-2790/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (708)470-6501
/ TELEFAX: (708)470-6881
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 777 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-08-762-227A-55

Query Match 61.9%; Score 283.6; DB 3; Length 777;
Best Local Similarity 81.6%; Pred. No. 5.8e-53;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 34 TCCGGCATCGAGGGCGCATGGCGCGCAGCGCGAGCCCGTCCACCCAGCGCGTGG 93
Db 376 TCTGGCGGGCGTCCAAACATGGCACCAGGCTGTTCCCGTCCCGTCTACCCAGCGCGTGG 435
QY 94 GAGCAGCTGAACCGCATCCAGGAGGCGCGAGGCTCTCTCAACCTCTCCCGCGACACCGCC 153
Db 436 GAACACGTGAATGCCATCCAGGAGGCGCGCGTCTCTCTGAACCTGAGTAGAGACACTGCT 495
QY 154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTGGATCTCCAGGAGCGGACC 213
Db 496 GCTGAGATGAATGAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCGGACT 555
QY 214 TGCCTCCAGACCGCTCGAGCTGTACAGCAGGCGCTCCGCGCGAGCCTCACCAAGCTC 273
Db 556 TGCCTACAGACCGCTCGAGCTGTACAGCAGGCGCTCGGCGGAGCCTCACCAAGCTC 615
QY 274 AAGGGCCCGCTCACCATGTATGGCGTCCCACTACAAGCAGCACTGCCACCGACCCCGGAG 333
Db 616 AAGGGCCCGCTTGACCATGTATGGCGCAGCACTACAAGCAGCACTGCCCTCCAAACCCCGGAA 675
QY 334 ACCTCTGCGCCACCCAGATCATCAGCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
Db 676 ACTTCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTC 735
QY 394 CTCTCGTGATCCGCTTCGACTCTGGAGCGGTCAGGAG 435
Db 736 CTGCTGTCTATCCCTTTGACTCTGGAGCCAGTCCAGGAG 777

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2005, 15:19:06 ; Search time 2523 Seconds
(without alignments)
6909.804 Million cell updates/sec

Title: US-10-723-083-1
Perfect score: 458
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479089

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gssi: *
9: gb_gssi2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	276.8	60.4	660	2	BE218982
3	276.8	60.4	666	1	AI912784
4	276.8	60.4	672	2	BE671554
5	276.8	60.4	695	2	BE669962
6	276.8	60.4	895	2	BE873976
7	276.2	60.3	658	5	BX111836
8	273.2	60.1	584	7	CF341802
9	273.6	59.7	592	7	CF370966
10	268.8	58.7	585	7	CF370833
11	264.8	57.8	718	6	CD369973
12	258.8	56.5	701	5	B0633411
13	256.4	56.0	565	2	BF938995
14	243.6	53.2	666	6	CA307828
15	230.8	50.4	661	6	CD368851
16	225.4	49.2	475	1	AA995402
17	208.6	45.5	561	6	CB437551
18	207.2	45.2	672	7	CF614774
19	202.4	44.2	511	6	CB430266
20	200.2	43.7	608	6	CD367244
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22	191.2	41.7	336	2	AW951121
23	176.6	38.6	549	1	AI677936
24	175.2	38.3	423	2	AW784714

c	25	166	36.2	531	4	BG236310	BG236310 naf26a07.
c	26	139	30.3	274	1	AA361936	AA361936 EST71529
c	27	134	27.1	244	4	BG236058	BG236058 naf21n12.
c	28	119.2	26.0	647	2	BB533718	BB533718 BB533718
c	29	114.4	25.0	517	6	CB430980	CB430980 606916 MA
c	30	104.8	22.9	269	7	CF370885	CF370885 TGESTVJ5
c	31	103.6	22.6	369	5	BX521029	BX521029 BX521029
c	32	102.6	22.4	483	1	AI180669	AI180669 uc47d08.r
c	33	96.4	21.0	629	2	BB664267	BB664267 BB664267
c	34	88.8	19.4	470	1	AI121878	AI121878 ud13c11.r
c	35	69	15.1	892	9	CR059250	CR059250 Forward S
c	36	67	14.6	1138	2	BE636680	BE636680 rockefell
c	37	63.8	13.9	697	9	AG112609	AG112609 Pan trogl
c	38	59.8	13.1	457	5	BQ620656	BQ620656 Tslr1135H
c	39	59	12.9	160	7	CF341980	CF341980 TGESTVJ5
c	40	59	12.9	925	9	CNS0091P	CNS0091P ZmombLa001
c	41	58.2	12.7	830	9	CM010233	CM010233 ZmombLa001
c	42	58	12.7	136	7	CF341168	CF341168 TGESTVJ4
c	43	57.8	12.6	881	9	CG339578	CG339578 QGWB73TV
c	44	57	12.4	747	9	CL959870	CL959870 OSIFCC036
c	45	56.8	12.4	671	6	CD926036	CD926036 G750.119N

ALIGNMENTS

RESULT 1
AW207707
LOCUS UI-H-BI2-age-e-09-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
DEFINITION IMAGE:2724184 3', mRNA sequence.
ACCESSION AW207707 588 bp mRNA linear EST 02-DEC-1999
VERSION AW207707.1 GI:6507203
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Oligo-dT track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Scores Lab Clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=No.

FEATURES
source

Location/Qualifiers
1..588
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2724184"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub4"
/notes="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NCI CGAP Sub4 library is a subtracted library derived from
the NCI CGAP Sub2 library which is a subtracted library
derived from the NCI CGAP Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP Co4, NCI_CGAP Pr22, NCI_CGAP
NCI_CGAP Co10, NCI_CGAP Co16, NCI_CGAP Kids,
NCI_CGAP Kid12, NCI_CGAP Kid3, NCI_CGAP Kid1,
NCI_CGAP Lym2, NCI_CGAP Br2, NCI_CGAP Co8, NCI_CGAP CLL1,
NCI_CGAP Le12, NCI_CGAP Brn2, NCI_CGAP Lu5,
NCI_CGAP Lu24, NCI_CGAP Lu19, NCI_CGAP GC4, NCI_CGAP GC6,

NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI CGAP Kid3 pool 1 : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI CGAP Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493255)

NCI CGAP Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Co10 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144594-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]

Tag Tissue=colon
TAG_LIB=NCI CGAP_Co4
TAG_SEQ=CTTCG"

ORIGIN

Query Match 60.4%; Score 276.8; DB 2; Length 588;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 8 GGATGACACCAACCACCACTCTCCGGCATCGAGGCGCGCATGGCGCCAGCGCGCA 67
DB 41 GGCTGCAGAGCCTGCTCTTGGGCACCTGGCCCTGCAGCATCTCTGCACCGCCGCT 100
QY 68 GCCGAGCCCGTCCACCCAGCCGTGGAGACGCTGAACGGATCCAGAGGCCCGCAGGC 127
DB 101 CGCCAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATCCATCCAGGAGCGCCGCGTC 160
QY 128 TCCTCAACTCTCCCGGACACCGCCGAGATGAACGAGCCGCGGAGGTGATCTCCG 187
DB 161 TCCTGAACCTGTAGAGACATCTGCTGTGATGAATGAACAGTAGAAGTATCTCAG 220
QY 188 AGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGCTGTACAAGCAG 247
DB 221 AATGTTTTCACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAAGCAG 280
QY 248 GCCTCGGCGGACCTTACCAAGCTCAAGGCCCGCTCACCATGATGGCGTCCCACTACA 307
DB 281 GCCTCGGCGGACCTTACCAAGCTCAAGGCCCGCTTGAACATGATGGCGGACCTACA 340
QY 308 AGCAGCACTGCCACACCGCCGAGACCTCTGCGCCACCCAGATCATCACCCTTCGAGA 367
DB 341 AGCAGCACTGCCCTTCAACCCCGGAACCTTCCTGTGAACCCAGATATCACCTTTGAAA 400
QY 368 GCTTCAAGGAGAACCTCAAGGACTTCTCTCTGTGATCCCGTTTCGACTGCTGGAGCCGG 427
DB 401 GTTTCAGAGAACCTCAAGGACTTCTCTCTGTGATCCCGTTTCGACTGCTGGAGCCAG 460
QY 428 TGACGAGGTGAG 439
DB 461 TCCAGGAGGTGAG 472

RESULT 2

BE218982 660 bp mRNA linear EST 03-JUL-2000
LOCUS hv47a07.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3176532 3'
DEFINITION similar to gb:M1220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
FACTOR PRECURSOR (HUMAN); mRNA sequence.
ACCESSION BE218982
VERSION BE218982.1 GI:8906300
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 660)

NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found at image.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 445.

FEATURES

Location/Qualifiers

1..660

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3176532"

/tissue_type="carcinoid"

/lab_host="DH10B"

/clone_lib="NCI CGAP Lu24"

/note="Organ: lung; Vector: p773D-Pac (Pharmacia) with a

modified polylinker; Plasmid DNA from the normalized

library NCI CGAP Lu5 was prepared, and ss circles were

made in vitro. Following HAP purification, this DNA was

used as tracer in a subtractive hybridization reaction.

The driver was PCR-amplified cDNAs from a pool of 5,000

clones made from the same library (clonoids

1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 60.4%; Score 276.8; DB 2; Length 660;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 8 GGATGACACCAACCACCACTCTCCGGCATCGAGGCGCGCATGGCGCCAGCGCGCA 67
DB 9 GGCTGCAGAGCCTGCTCTTGGGCACCTGGCCCTGCAGCATCTCTGCACCGCCGCT 68
QY 68 GCCGAGCCCGTCCACCCAGCCGTGGAGACGCTGAACCGCATCCAGGAGGCCCGCAGGC 127
DB 69 CGCCAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGCGTC 128
QY 128 TCCTCAACTCTCCCGGACACCGCCGAGATGAACGAGCCGCTCGAGCTGTACAAGCAG 187
DB 129 TCCTGAACCTGTAGTAGACACTGCTGCTGTGATGAATGAACAGTAGAAGTATCTCAG 188
QY 188 AGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTTCGAGCTGTACAAGCAG 247
DB 189 AATGTTTTCACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAAGCAG 248
QY 248 GCCTCGGCGGACCTTACCAAGCTCAAGGCCCGCTTCAACATGATGGCGTCCCACTACA 307
DB 249 GCCTCGGCGGACCTTACCAAGCTCAAGGCCCGCTTGAACATGATGGCGGACCTACA 308
QY 308 AGCAGCACTGCCACCGCCGAGACCTCTGCGCCACCCAGATCATCACCCTTCGAGA 367
DB 309 AGCAGCACTGCCCTTCAACCCCGGAACCTTCCTGTGTGAACCCAGATATCACCTTTGAAA 368
QY 368 GCTTCAAGGAGAACCTCAAGGACTTCTCTCTGTGATCCCGTTTCGACTGCTGGAGCCGG 427
DB 369 GTTTCAGAGAACCTCAAGGACTTCTCTCTGTGATCCCGTTTCGACTGCTGGAGCCAG 428
QY 428 TGACGAGGTGAG 439

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Db          429  TCCAGGAGTGAG 440
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RESULT 3
AI912784
LOCUS
DEFINITION
AI912784        666 bp      mRNA          linear      EST 18-DEC-1999
we13f07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340997 3'
similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
FACTOR PRECURSOR (HUMAN);, mRNA sequence.
AI912784
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lemmon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 743 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 447.

FEATURES
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/clone="IMAGE:2340997"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonesIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match          60.4%; Score 276.8; DB 1; Length 666;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY      8  GGATGACACACACACACACCTCTCTCGGATCGAGGCCGCATGCGCGCAGCGCA 67
Db      9  GGCTGCAGAGCCCTGCTCTTGGGCACTGTGGCCCTGCAGCATCTCTGCACCGCCCGCT 68
QY     68  GCCCGAGCCGTCACCCAGCCGTGGAGCAGCTGAACGGATCCAGGAGGCCCGCAGGC 127
Db     69  CGCCAGCCCGCAGCAGCAGCCCTGGAGCATGTGATGCCATCCAGAGGCCCGCGTC 128
QY    128  TCCTCAACCTCTCCCGCAGCACCGCCCGCAGATGAACGAGACCGGTGAGGTGATCTCCG 187
Db    129  TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAGTATCTCAG 188
QY    188  AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCGCCCTCGAGCTGTGTACAAGAGG 247
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Db          189  AAATGTTTGACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAAGCAGG 248
QY     248  GCCTCCGGCGAGCCTTCACAAAGCTCAAGGGCCCGCTCACCATTGATGGCGTCCCACTACA 307
Db     249  GCCTGGGGGAGCCTTCACAAAGCTCAAGGGCCCGCTTGACCATGATGGCGCAGCTACA 308
QY     308  ACAGCACTGCCACCGACCGCCGAGACCTCTCGGCCACCCAGATCATCACTTCGAGA 367
Db     309  AGCAGCACTGCCCTCCAAAGCCCGGAACCTTCCTGTGCAACCCAGATTATCACCTTTGAA 368
QY     368  GCTTCAAGGAGAACCTCAAGGACTTCTCTCTCTGATCCGTTTCGACTGCTGGAGCGG 427
Db     369  GTTCAAGAGAACCTCAAGGACTTCTCTCTGTCATCCCTTTGACTGCTGGAGCCAG 428
QY     428  TCCAGGAGTGAG 439
Db     429  TCCAGGAGTGAG 440
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RESULT 4
BE671554
LOCUS
DEFINITION
BE671554        672 bp      mRNA          linear      EST 08-SEP-2000
7e53h07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3286237 3'
similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
FACTOR PRECURSOR (HUMAN);, mRNA sequence.
BE671554
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 672)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lemmon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 440.

FEATURES
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/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonesIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match          60.4%; Score 276.8; DB 2; Length 672;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
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QY	8	GGATGCACCA	CCACCA	CCACCA	CTCTCTCCG	GCATCGAGG	CCGCATG	CGCCAGCGCGCA	67
Db	16	GGCTGCAGAG	CGCTCTG	CTTTGGG	CACTGTGG	CGCTGCAG	CATCTCTC	ACCCGCCCGCT	75
QY	68	GCCCGAGC	CGGTCC	ACCCAG	CGCTGG	GAGCAGTGA	ACGCGCAT	CCAGGAGCGCCG	127
Db	76	CGCCAGCC	CCAGCAG	CGCCCTGG	NGCATGTGA	TGCCAT	CCAGGAGCGCCG	CGTC	135
QY	128	TCCTCAAC	TCTCC	CGGACA	CCCGCCG	CGAGATGA	ACGAGAC	CGGTGGAGTGAT	187
Db	136	TCCTGAAC	CTGAGT	AGAGACA	CTGCTGTG	AGATGAATGA	AACAGTAGA	AGTCTCTCAG	195
QY	188	AGATGTT	TCGATTC	CCAGSAG	CGCACTGC	CTCCAGAC	CCGCGCTCG	AGCTGTAC	247
Db	196	AAATGTT	TGACCT	CCAGAG	CGGACCTGC	CTACAGAC	CCGCGCTG	GAGCTGTAC	255
QY	248	GCCTCCG	CGGAGC	CTCACC	AAAGTCTCA	AGGCGCG	CGCTCACC	ATGATGGCGT	307
Db	256	GCCTGCG	GGGAGC	CTCACC	AAAGTCA	AGGCGCC	CTTGAC	CATGATG	315
QY	308	AGCAGCA	CTGCCAC	CGACCC	CGGAGAC	CTCTCTGG	CCACCCAGAT	CATCACTTC	367
Db	316	AGCAGCA	CTGCCCT	CCAA	CCCGGAA	ACTTCCTGT	GCAACCCAGAT	TATCACTTTG	375
QY	368	GCTTCA	AGGAGAA	CGCTCA	AGGACTTC	CTCTCTCG	TGATCC	CGTTCGAC	427
Db	376	GTTTCA	AGAGAA	CGTGA	AGGACTTT	CTGCTGT	GTGATCC	CCCTTTGAC	435
QY	428	TGCAGG	AGTGAG	439					
Db	436	TCCAGG	AGTGAG	447					

RESULT	5
BE66962	
LOCUS	B5669962
DEFINITION	7827908.x1 NCI CGAP Lu24 Homo sapiens CDNA clone IMAGE:3283742 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN) ; mRNA sequence.
	695 bp mRNA linear EST 08-SEP-2000

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FEATURES
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high quality sequence stop: 456.
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a

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modified polylinker: plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made *in vitro*. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1532439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

RESULT	6
BE873976	
LOCUS	
DEFINITION	BE873976 Homo sapiens CDNA clone IMAGE:388651 5' , mRNA linear EST 20-OCT-2000 601484045F1 NIH_MGC_69 Homo sapiens CDNA clone IMAGE:388651 5' , mRNA sequence.
ACCESSION	BE873976
VERSION	GI:10322752
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 895) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: DCTD/BTP/Gazdar CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9663 row: j column: 12

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High quality sequence stop: 711.
FEATURES
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        /clone="IMAGE:388571"
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        /lab_host="DH10B (phage-resistant)"
        /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
ORIGIN
  Query Match      60.4%; Score 276.8; DB 2; Length 895;
  Best Local Similarity 77.5%; Pred. No. 7.1e-50;
  Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 8 GGATGACACACACACACACACCTCTCCGGCATCGAGGCCCGCATGGCGCCAGCGCGCA 67
DB 1 |||||
QY 68 GCCCGAGCCGTCACCCAGCCGTGGAGCAGCTGACGACGATCCAGGAGCCCGCAGGC 127
DB 3 GGCTGACAGACCTGCTGCTTGGGCACCTGGCGCTGCAGCATCTCTGCACCGCCCGCT 62
QY 63 CGCCAGCCCGCAGCAGCAGCCCTGGAGCATGTGAATCCATCCAGGAGGCCCGCGTC 122
DB 1 |||||
QY 128 TCCTCAACCTCTCCCGCGACACCGCCGCGAGATGAACGAGACCGTGGAGGTATCTCCG 187
DB 1 |||||
QY 123 TCCTGAACCTGAGTAGAGACACTGCTGTGAGATGATGAACAGTAGAGTATCTCAG 182
QY 188 AGATGTTGATCTCAGGAGCCGACCTGCTCCAGACCCCGCTCGAGCTGTATAAGCAGG 247
DB 183 AAATGTTTACCTCCAGGAGCCGACCTGCCTACAGACCCCGCTGGAGCTGTACAAGCAGG 242
QY 248 GCTCTCGCGCAGCCTCACAAGCTCAAGGCGCGCTCACCATTGATGGGTCCCATACA 307
DB 243 GCTTCGGGGCAGCCTCACAAGCTCAAGGCGCGCTTGAACATGATGGCGCAGCATACA 302
QY 308 AGCAGCACTGCCACACGACCCCGAGACCTCTCCGCGCACCCAGATCATCACCTTCGAGA 367
DB 303 AGCAGCACTGCCCTCCAAACCCCGGAACTTCCTGTGCAACCCAGATTATCACCTTTGAA 362
QY 368 GCTTCAAGGAGACCTCAAGGACTTCTCTCTGTGATTCCTGTTGAGTTCGAGTGGAGCCGG 427
DB 363 GTTTCGAAGAGAACCTCAAGGACTTCTCTGTGATTCCTGTTGAGTTCGAGTGGAGCCAG 422
QY 428 TGCAGGAGTGAG 439
DB 423 TCAGGAGTGAG 434
RESULT 7
BX111836/c 658 bp mRNA linear EST 07-FEB-2003
LOCUS
DEFINITION
  BX111836 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE998C104061 ;
  IMAGE:1601601, mRNA sequence.
ACCESSION
  BX111836
VERSION
  BX111836.1 GI:27837278
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 658)
    Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
    Radelof,U., Schneider,D. and Korn,B.
  Human Unigeneset - RZPD3
  Unpublished (2003)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998C104061.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.
FEATURES
  Location/Qualifiers
    1..658
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:1601601"
      /tissue_type="carcinoid"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Lu5"
      /notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
      modified polylinker; 1st strand cDNA was prepared from
      neuroendocrine lung carcinoid, and was then primed with a
      Not I - oligo(dT) primer. Double-stranded cDNA was ligated
      to Eco RI adaptors (Pharmacia), digested with Not I and
      cloned into the Not I and Eco RI sites of the modified
      pT7T3 vector. Library is normalized. Library was
      constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
  Query Match      60.3%; Score 276.2; DB 5; Length 658;
  Best Local Similarity 82.3%; Pred. No. 9.5e-50;
  Matches 317; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 55 GCGCCAGCGCGCAGCCGCGCTCCACCCAGCCCTGGGAGCACCTGAACGCGATCCAG 114
DB 619 GCACCCGCGCGCTCGCGCCAGCCCGCCAGCGACGCGCATGTGAATGCCATCCAG 560
QY 115 GAGGCGCGCAGGCTCTCTCAACCTCTCCCGCGACACCGCCGCGAGATGAACGAGACCGTG 174
DB 559 GAGGCGCGCGCTCTCTGAACTGTAGTAGACACTGCTGTGAGATGAATGAACAGTA 500
QY 175 GAGGTGATCTCGAGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCCGCTCGAG 234
DB 499 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCTCAGACCCCGCTGGAG 440
QY 235 CTGTACAAGCAGCGGCTCCGCGCAGCCTCACCAGCTCAAGGCGCGCTCAGCATGATG 294
DB 439 CTGTACAAGCAGCGGCTCGCGGCGACGCTCAACAGCTCAAGGGCGCTTGAACCATGATG 380
QY 295 GGTCTCCACTACAAGCAGCAGCTGCCCGACCGACCCCGGAGACCTCTCTGCGCACCCAGATC 354
DB 379 GCAGCAGCATACAAGCAGCAGCTGCCCTCCAAACCCCGGAACTTCTCTGTGCAACCCAGATT 320
QY 355 ATCAGCTTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCTCTCTGTGATCCCGTTCGAC 414
DB 319 ATCAGCTTGTAAAGTTCAAAGAGAACCTGAAGGACTTCTCTGTCTGTCTATCCCTTTGAC 260
QY 415 TGCTGGAGCCCGGTGCAGGAGTGAG 439
DB 259 TGCTGGAGCCAGTCCAGGAGTGAG 235
RESULT 8
CF341802 584 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION
  T9ESTzyj43f02.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
  cDNA clone T9ESTzyj43f02.y1 5' similar to SW:CSF2 HUMAN P04141
  GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
  sequences.
ACCESSION
  CF341802
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ORIGIN
Query Match
Best Local
Matches 334; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

CF341802.1 GI:33831915
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
1 (bases 1 to 584)
Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioaka,J.A., White,M.,
Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxost@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..584
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTzyj43f02.y1"
/dev_stage="Tachyzoite"
/lab_host="Electroten Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/notes="Vector: Modified pBluescript (pBS SK+); Site 1:
BamHI; Site 2: EcoRI; The cDNA library was constructed by
Keliang Tang, and Robert Cole at Washington University.
cDNA was synthesized from poly(A)+ mRNA using the
template-switching PCR method (SMART cDNA Kit, BD
Biosciences). First strand cDNA was reverse transcribed
using the CDS III/3' primer and a 5' template switch
primer (Smart IV primer). The product of the first strand
synthesis was PCR amplified using the same primer set and
the fragments were digested with SfiI. The fragments were
size selected, ligated into a modified pBluescript vector
(obtained from Michael White, Montana State University)
containing directional SfiI sites, and electroporated into
ElectroTen Blue cells. Vector: SfiI sites were added to
the multiple cloning region of pBluescript SK+ between the
BamHI/EcoRI sites. The modified polylinker has the
following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--
GGCGGCTCGCCACGGATCC3' where n=3-4 G nucleotides.
WARNING: the library contains a small percentage of cDNAs
derived from the human host cells. Library materials
provided by David Sibley, Washington University."

8 GGATGACACACACACACACACCTCTCTCGGCATCGAGGCGCCATGGCGCCAGCGCA 67
37 GGCTGCAGAGCCTGTGCTTTGGGCACTGTGGCTTCGACATCTCTGCACCGCCGCGCT 96
68 GCCGAGCCGCTCCACCCAGCCTGGGAGCACTGTACCGATCCAGGAGCCCGCAGCG 127
97 CGCCCCAGCCCCAGCAGCAGCCCTGGGAGATGTGAATGCATCCAGGAGGCCCGCGTC 156
128 TCCTCAACCTCTCCCGCGACACCGCCGCGAGATGAACAGACCGCTGGAGGTATCTCCG 187
157 TCCTGAACCTGATAGAGACACTGCTGCTGAGATGATGAATGAACAGTAGATCTCTAG 216
188 AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCCGCTTCGAGCTGTACAGAGG 247

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Db 217 AAATGTTTTCACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGTACAGCAGG 276
QY 248 GCTTCGCGCGAGCCTCACCAGCTCAAGGCGCCGCTCACCATGATGGCGTCCACTACA 307
Db 277 GCTTCGCGCGAGCCTCACCAGCTCAAGGCGCCGCTTGTGCAACCCAGACTATCAG 336
QY 308 AGCAGCACTGCCACCGACCGACCGCGGAGACCTCTCTGGCCACCCAGATCATCATTCGAGA 367
Db 337 AGCAGCACTGCCCTCCAAACCCCGGAACTTCTGTGCAACCCAGACTATCAGCTTGAA 396
QY 368 GCTTCAAGAGAACCTCAAGGACTTCTCTCTCGTATCCCGTTCGACTGCTGGAGCCGG 427
Db 397 GTTTCAGAGAACCTCAAGGACTTCTCTCTGTGTCATCCCTTGTGCTGCGGAGCCAG 456
QY 428 TGCAGGAGTGAG 439
Db 457 TCAGGAGTGAG 468

RESULT 9
CF370966
LOCUS
DEFINITION
592 bp mRNA linear EST 27-AUG-2003
TgESTzyj58e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
cDNA clone TgESTzyj58e12.y1 5' similar to SW:CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ; , MRNA
sequence.
CF370966
CF370966.1 GI:34318212
EST.
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
1 (bases 1 to 592)
Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioaka,J.A., White,M.,
Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxost@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..592
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTzyj58e12.y1"
/dev_stage="Tachyzoite"
/lab_host="Electroten Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/notes="Vector: Modified pBluescript (pBS SK+); Site 1:
BamHI; Site 2: EcoRI; The cDNA library was constructed by
Keliang Tang, and Robert Cole at Washington University.
cDNA was synthesized from poly(A)+ mRNA using the
template-switching PCR method (SMART cDNA Kit, BD
Biosciences). First strand cDNA was reverse transcribed
using the CDS III/3' primer and a 5' template switch
primer (Smart IV primer). The product of the first strand
synthesis was PCR amplified using the same primer set and
the fragments were digested with SfiI. The fragments were
size selected, ligated into a modified pBluescript vector
(obtained from Michael White, Montana State University)
containing directional SfiI sites, and electroporated into
ElectroTen Blue cells. Vector: SfiI sites were added to
the multiple cloning region of pBluescript SK+ between the
BamHI/EcoRI sites. The modified polylinker has the
following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--
GGCGGCTCGCCACGGATCC3' where n=3-4 G nucleotides.
WARNING: the library contains a small percentage of cDNAs
derived from the human host cells. Library materials
provided by David Sibley, Washington University."

```


containing directional SfiI sites, and electroporated into ElectroTen Blue cells. Vector: SfiI sites were added to the multiple cloning region of pBluescript SK+ between the BamHI/EcoRI sites. The modified polylinker has the following sequence: 5'-GAATTCGGCCATTACGGCC(G)n-- insert--GGCCGCTCGGCCACGAGATCC3' where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."

ORIGIN

Query Match 59.7%; Score 273.6; DB 7; Length 592;
Best Local Similarity 77.1%; Pred. No. 3.5e-49;
Matches 333; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 8 GGATGCACCAACCAACCACTCTCTCGGCATCGAGGCGCATGGCCCGCCAGCGCA 67
|||||
Db 39 GGATGCAGAGCCTGTCTCTTGGCAGCTGTGGCTGCAGCATCTCTGCACCCGCCGCT 98
|||||
QY 68 GCCGAGCCGCTCACCAAGCCTGGGAGCAGCTGAACGGATCCAGGAGCCCGCAGGC 127
|||||
Db 99 CGCCAGCCCGCAGCAGCAGCCCTGGGAGCATGTGAATGCATCCAGGAGCCCGCGTC 158
|||||
QY 128 TCCTCAACCTCTCCCGCAGCACCGCCGAGATGAACGAGACCGTGGAGTGATCTCG 187
|||||
Db 159 TCTGAACCTGTAGAGACACTGTCTGAGATGAATGATATAGTAGAAGTCACTTCAG 218
|||||
QY 188 AGATGTTTCGATCTCCAGGAGCCGACCTCTCCAGACCCCGCTCGAGCTGTACAAAGCAGG 247
|||||
Db 219 AAATGTTTGACCTCCAGGAGCCGACCTGCTACAGACCCCGCTGGAGCTGTACAAAGCAGG 278
|||||
QY 248 GCTTCGCGGCGAGCTTACCAAGCTCAAGGCGCCGCTACCATGATGGCGTCCCACTACA 307
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Db 279 GCCTGGGGGAGCGCCACCAAGCTCAAGGCGCCCTTGACCATGTCGCGCAGCCACTACA 338
|||||
QY 308 AGCAGCACTGCCACCGACCCCGAGACCTCTCGGCCACCCAGATCATCACTTCGAGA 367
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Db 339 AGCAGCACTGCCCTCCAAACCCCGAACTTCCTGTGCAACCCAGACTATCACTTTGAA 398
|||||
QY 368 GCTTCAAGGAGAACCTCAAGGAGCTTCTCTCTCGTGATCCCGTTCGACTGTGGAGCCGG 427
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Db 399 GTTTCAAAGAGACCTCAGAGACTTCTGCTGTGATCCCTTGTACTGCTGGAGCCAG 458
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QY 428 TGAGAGGTGAG 439
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Db 459 TCCAGAGGTGAG 470
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RESULT 10

CF370833

LOCUS

DEFINITION

CF370833 585 bp mRNA linear EST 27-AUG-2003
TgESTzyj55el2.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
cDNA clone TgESTzyj55el2.y1 5' similar to SW.CSF2 HUMAN P04141
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ; mRNA
sequence.

CF370833

VERSION

CF370833.1

KEYWORDS

SOURCE

ORGANISM

Toxoplasma gondii

Toxoplasma gondii

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Toxoplasma.

1 (bases 1 to 585)

Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M.,

Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,

Hiller, L., Kucaba, R., Theising, B., Bowers, I., Gibbons, M.,

Ritter, E., Bennett, J., Franklin, C., Teagareishvili, R., Ronko, I.,

Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.

Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.

Toxoplasma EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@wustl.edu
Contact David Sibley (toxost@porcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40UP from Gibco.

FEATURES

source

1..585

/organism="Toxoplasma gondii"

/mol_type="mRNA"

/db_xref="taxon:5811"

/clone="TgESTzyj55el2.y1"

/dev_stage="Tachyzoite"

/lab_host="ElectroTen Blue cells (Stratagene)"

/notes="Vector: Modified pBluescript (pBS SK+); Site 1:

BamHI, Site 2: EcoRI; The cDNA library was constructed by

Keliang Tang, and Robert Cole at Washington University.

cDNA was synthesized from poly(A)+ mRNA using the

template-switching PCR method (SMART cDNA Kit, BD

Biosciences). First strand cDNA was reverse transcribed

using the CDS III/3' primer and a 5' template switch

primer (Smart IV primer). The product of the first strand

synthesis was PCR amplified using the same primer set and

the fragments were digested with SfiI. The fragments were

size selected, ligated into a modified pBluescript vector

(obtained from Michael White, Montana State University)

containing directional SfiI sites, and electroporated into

ElectroTen Blue cells. Vector: SfiI sites were added to the

multiple cloning region of pBluescript SK+ between the

BamHI/EcoRI sites. The modified polylinker has the

following sequence: 5'-GAATTCGGCCATTACGGCC(G)n-- insert--

GGCCGCTCGGCCACGAGATCC3' where n=3-4 G nucleotides.

WARNING: the library contains a small percentage of cDNAs

derived from the human host cells. Library materials

provided by David Sibley, Washington University."

ORIGIN

Query Match 58.7%; Score 268.8; DB 7; Length 585;
Best Local Similarity 76.4%; Pred. No. 3.8e-48;
Matches 330; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 8 GGATGCACCAACCAACCACTCTCTCGGCATCGAGGCGCGCATGGCCCGCCAGCGCA 67
Db 39 GGCTGCAGAGCCTGTCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCCGCT 98
|||||
QY 68 GCCGAGCCGCTCCACCGAGCCGTGGAGCAGCTGAACGGATCCAGGAGCCCGCAGGC 127
|||||
Db 99 CGCCAGCCCGCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGCCCGCGTC 158
|||||
QY 128 TCTCAACCTCTCCCGCAGCACCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
|||||
Db 159 TCTGAACCTGTAGTAGAGACACTGTCTGTGAGATGAATTTATAGTAGAAGTCACTTCAG 218
|||||
QY 188 AGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCCGCTCGAGCTGTACAAAGCAGG 247
|||||
Db 219 AAATGTTTGACCTCCAGGAGCCGACCTGCTACAGACCCCGCTGGAGCTGTACAAAGCAGG 278
|||||
QY 248 GCTTCGCGGCGAGCTTACCAAGCTCAAGGCGCCGCTTCACTATGATGGCGTCCCACTACA 307
|||||
Db 279 GCCTGGGGGAGCGCCACCAAGCTCAAGGCGCCCTTGACCATGATGGCCAGCCACTACA 338
|||||
QY 308 AGCAGCACTGCCACCGACCCCGAGACCTCTCGGCCACCCAGATCATCACTTCGAGA 367
|||||
Db 339 AGCAGCACTGCCCTCCAAACCCCGAACTTCCTGTGCAACCCAGACTATCACTTTGAA 398
|||||
QY 368 GCTTCAAGGAGAACCTCAAGGAGCTTCTCTCTGTGATCCCGTTCGACTGCTGGAGCCGG 427
|||||
Db 399 GTTTCAAAGAGAACCTGAAGGAGCTTCTCTGTGATCCCTTTGACTGCTGGAGCCAG 458
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QY 428 TGAGAGGTGAG 439
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Db      459 TCCAGGAGTGAG 470

RESULT 11
CD369973/c
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD369973      718 bp mRNA linear EST 05-AUG-2004
UI-H-FTI-bke-o-08-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
UI-H-FTI-bke-o-08-0-UI 3', mRNA sequence.
CD369973
CD369973.1 GI:31154063
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 65-134, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLVA=Yes.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bke-o-08-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTI"
/noted="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP) moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP) moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
p773-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
```

ORIGIN

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Query Match      57.8%; Score 264.8; DB 6; Length 718;
Best Local Similarity 82.3%; Pred. No. 2.8e-47;
Matches 316; Conservative 0; Mismatches 67; Indels 1; Gaps 1;

QY      56 CGCCAGCGGAGCCGCGCTCCACCCAGCCGCTGGAGACCTGACGATCCAGG 115
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      718 CACCCGCGCGCTCGCCAGCCCGCCAGCAGCCCTGGAGCATGTGATGCCATCCAGG 659
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      116 AGCCCGCGGAGGCTCTCAACCTCTCCCGCGACACCGCCCGAGATGACGAGACCGTG 175
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      658 AGCCCGCGGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAG 599
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      176 AGTGATCTCCAGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGC 235
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      598 AAGTCATCTCAGAAATGTT-GACCTCCAGGAGCCGACCTGCTTACAGACCCGCTGGAGC 540
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      236 TGTACAAGCAGGCGCTCCGCGCAGCCTCAACCAAGCTCAAGGCGCGCTCAACCATGATG 295
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      539 TGTACAAGCAGGCGCTCCGCGCAGCCTCAACCAAGCTCAAGGCGCGCTTGAACATGATG 480
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      296 CGTCCCACTTACAAGCAGCAGCTCCCAACCGACCCCGGAGACCTCTCGCGCCACCCAGATCA 355
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      479 CCAGCCACTTACAAGCAGCAGCTCCCTCCAAACCCCGGAACTTCTGTGCAACCCAGATTA 420
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      356 TCACCTTGAGAGCTTCAAGGAGAACCTCAAGGACTTCTCTCTGATGATCCCGTTGACT 415
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      419 TCACCTTTGAAAGTTTCAAGAGAAACCTTGAGGACTTTCTGCTTGTCTATCCCTTTGACT 360
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      416 GCTGGAGCGCGCTCGCAGGAGTGAG 439
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      359 GCTGGAGCGCAGTCCAGGAGTGAG 336
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 12

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BU633411/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BU633411      701 bp mRNA linear EST 23-SEP-2002
UI-H-FTI-bgu-1-15-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
UI-H-FTI-bgu-1-15-0-UI 3', mRNA sequence.
BU633411.1 GI:23300666
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bent-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT rich#Low_complexity 60-129,
>(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLVA=Yes.

FEATURES
source
Location/Qualifiers
1..701
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapso@ncim.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Prepared by: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 497.
Location/Qualifiers
1. .565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3706893"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI-CGAP Lu24"
/notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonesIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Ronaldo."

```

/clonename="UI-H-FL1-bgu-l-15-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FL1"
/note="Organ: Chondrosarcoma; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FL1 is a normalized cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGTCGGTG. The cell lines were provided by Dr. James Martin from the University of Iowa."
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGTCGGTG"

ORIGIN

Query Match          56.5%; Score 258.8; DB 5; Length 701;
Best Local Similarity 83.0%; Pred. No. 5.7e-46;
Matches 307; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

Qy      70   CCAGGCCCGCTCCACCCAGCCGTTGGGACACGTGAACCGCATCCAGGAGGCCCGCAGGCCTC 129
        |||||
Db      699  CCACGCCCCAGCACGACGCCGTTGGGACATGTGAA-TCCATCCAGGAGGCCCGCGCTC 641

```

ORIGIN

Scores and M: Racima Bonarao.

	Query Match Best Local Similarity Matches	56.0%; 77.4%; 336;	Score 256.4; Pred. No. 1.9e-45; Conservative	DB 2; Mismatches 0; Indels 2;	Length 565; Gaps 2;
Qy	8	G G A T G C A C C A C C A C C A C C A C T C T C C G G C A T C G A G G G C C G C A T G G C G C C A G C G G C G C A	67		
D b	45	G G C T G C A G A G C C T G C T G C T C T T G G G C A C T G T G C C T G C A G C A T C T C T G C A C C G C C G C T	104		
Qy	68	G C C C G A G C C C G T C C A C C C C A G - C G T G G G A C A C G T G A A C C G G A T C - C A G G A G C C C C G C A G	125		
D b	105	C G C C C A G C C C C A C A C G C A C G C C C G T G B G A C A T G T G A A T G C C A T C A C A G A G G C C C G C G C	164		
Qy	126	G C T C C T C A A C C T C T C C C G C A C A C C G C C G C G A G A T G A A C A G A C C C T G G A G G T G A T C T C	185		
D b	165	T C T C C T G N A C C T G A G T A G A G A C A C T G C T G T G A G A T G A T G A A C A G T A G A N G T C A T C T C	224		
Qy	186	C G A G A T T T G A T C T C A G G A G C C G A C C T G C C T C C A G A C C C G C C T C G A G C T G T A C A A G C A	245		
D b	225	A G A A A T G T T T G A C C T C C A G G A G C C G A C C T G C C T A C A G A C C C G C G T G A G C T G T A C A A G C A	284		
Qy	246	G S G C C T C C G G G A G C C T C A C A A G C T C A A G G C C C G C C T C A C C A T G A T G G G T C C C A C T A	305		
D b	285	G G G C C T C G G G G A G A G C C T C A C A A G C T C A A G S G C C C C T T G A C C A T G A T G C C A G C C A C T A	344		
Qy	306	C A A G C A G A C T G C C C A C C G A C C C C G G A G A C C T C C T G G G C C A C C C A G A T C A T C A C T T T C G A	365		
D b	345	C A A G C A G A C T G C C T C C A A C C C C G G A A C T T C C T G T G C A A C C C A G A N T A T A C C T T T G A	404		
Qy	366	G A C T T T C A A G G A A C C T C A A G G A C T T C C T C G T G A T C C C G T T C G A C T G C T G G G A G C C	425		
D b	405	A A G T T T C A A A G A A C C T G A A G A C T T T C G T T G T C A T C C C C T T T G A C T G C T G G G A G C C	464		
Qy	426	G T T G C A G G A G T G A G	439		
D b	465	A G T C C A G G A G T G A G	478		

[illegible]

NCI_CGAP_FTI1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FTI1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match	50.4%	Score 230.8;	DB 6;	Length 661;
Best Local Similarity	83.5%	Pred. No. 6.7e-40;		
Matches 273;	Conservative 0;	Mismatches 53;	Indels 1;	Gaps 1;

Qy	113	AGGAGCCCGCAGGCTCCTCAACCTTCGCGGACACCGCCGAGATGAACGAGACCG 172
Db	661	AGGAGCCCGCGCTCTCTGAACTGAGTAGACACACTGCTGCTGAGATGAATGAACAG 602
Qy	173	TGGAGGTGATCTCGAGATGTTGATCTCCAGGAGCGGACCTGCTCCAGACCCGCTCG 232
Db	601	TAGAAGTCATCTCAGAAATG-TNGACCTCCAGGAGCGGACCTGCTCCACAGACCCGCTCG 543
Qy	233	AGCTGTACAGCAGGCGCTCCGCGGAGCTCACCAGCTCAAGGCGCGCTCACCATGA 292
Db	542	AGCTGTACAGCAGGCGCTTCGCGGAGCGCTCACCAGCTCAAGGCGCGCTTGAACATGA 483
Qy	293	TGGCGTCCCACTACAAGCAGCACTGCGCACCGACCCCGGAGACCTCTCGCGCACCCAGA 352
Db	482	TGGCCAGCCACTACAAGCAGCACTGCGCTCCAACCCCGGAACTTCTGTGCAACCCAGA 423
Qy	353	TCATCAGCTTCGAGAGTTCAAGAGAACCTCAAGACTTCCTCTCGTGATCCCGTTG 412
Db	422	TTATCAGCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTCTGCTTGTCATCCCTTTG 363
Qy	413	ACTGCTGGGAGCGGTCGAGAGTGAG 439
Db	362	ACTGCTGGGAGCGGTCGAGAGTGAG 336

Search completed: March 11, 2005, 17:24:17
Job time : 2532 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2005, 09:51:36 ; Search time 420 Seconds
(without alignments)
6455.337 Million cell updates/sec

Title: US-10-723-083-1

Perfect score: 458

Sequence: 1 cggccggatgcaccacca.....gtagcgtagcagcatgccg 458

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319.2	69.7	905	2	AAQ03221 DNA fragm
2	318.4	69.5	896	2	AAQ03220 DNA fragm
3	315	68.8	386	2	AAQ03219 DNA fragm
4	312.6	68.3	435	12	ADI20788 Human GM-
5	311	67.9	435	12	ADI20790 Human GM-
6	284.4	62.1	435	12	ADG76023 Human GM-
7	283.6	61.9	777	2	AAQ97169 pMON13022
8	283.6	61.9	777	3	AAQ03723 Human int
9	283.6	61.9	777	6	ABX00012 Human int
10	283.6	61.9	777	12	ADJ14267 DNA relat
11	283	61.8	402	2	AAQ97208 pMON13012
12	283	61.8	402	3	AAQ03771 Human G-C
13	283	61.8	402	6	ABX00086 Human int
14	283	61.8	402	12	ADJ14388 DNA relat
15	281	61.4	822	2	AAQ97183 pMON13035
16	281	61.4	822	3	AAQ03737 Human int
17	281	61.4	822	6	ABX00026 Human int
18	281	61.4	822	12	ADJ14281 DNA relat
19	281	61.4	903	2	AAQ97180 pMON13031
20	281	61.4	903	3	AAQ03734 Human int

21	281	61.4	903	6	ABX00023 Human int
22	281	61.4	903	12	ADJ14278 DNA relat
23	277.8	60.7	1538	10	Adf31962 Human GM-
24	277.8	60.7	1538	10	Adf31989 Human gra
25	277.6	60.6	415	1	AAAN90383 Synthetic
26	277.6	60.6	415	1	AAAN90274 Synthetic
27	277	60.5	2211	12	ADL16719 Human stu
28	276.8	60.4	448	12	ADL16729 Human gra
29	276.8	60.4	763	2	AAQ04018 Granulocy
30	276.8	60.4	781	12	ADN07714 Human G-C
31	276.8	60.4	781	12	ADP10387 Reference
32	276.8	60.4	787	1	AAAN60364 Human gra
33	276.8	60.4	787	2	AAQ84865 Clone pCD
34	276.8	60.4	789	3	AAQ35017 Human ade
35	276.8	60.4	789	3	AAF21139 Human low
36	276.8	60.4	789	4	AAH28217 Nucleotid
37	276.8	60.4	789	10	ABZ96833 Human nuc
38	276.8	60.4	789	11	ABD20682 Human pul
39	276.8	60.4	2385	2	AAAT72725 Her2-GM-C
40	276.8	60.4	5115	3	AAA35020 Human ade
41	276.8	60.4	5115	3	AAF21142 Human low
42	276.8	60.4	5115	10	ABZ96836 Human nuc
43	276.8	60.4	5115	11	ABD20685 Human pul
44	276.8	60.4	9629	2	AAAT14600 pXJCL-hGM
45	276.2	60.3	1011	8	ABX63509 Human CDN

ALIGNMENTS

RESULT 1
AAQ03221
ID AAQ03221 standard; DNA; 905 BP.

XX AAQ03221;

DT 12-JUL-1990 (first entry)

DE DNA fragment of pABO-GMCSF encodes granulocyte macrophage colony stimulating factor (GM-CSF).

XX Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; da.

OS Streptomyces sp.

XX EP352707-A.

PD 31-JAN-1990.

XX 24-JUL-1989; 89EP-00113607.

XX 25-JUL-1988; 88CA-00572956.

XX (CANG-) CANGENE CORP.

PI Garvin RT, Malek LT;

DR WPI; 1990-031296/05.

PT gene expression system directing secretion of protein in Streptomyces - contg. structural gene, esp. for granulocyte macrophage colony stimulating factor, and regulatory sequence.

PS Disclosure; Fig 4; 39pp; English.

CC GM-CSF, or a wide range of other proteins, is secreted in unglycosylated form, with correctly positioned intramolecular disulphide bonds and full biological activity. pABO-GMCSF contains the BamHI HindIII fragment with an aminoglycoside phosphotransferase promoter and the protease B-endo H hybrid signal peptide. GM-CSF is potentially useful in cancer treatment

XX Sequence 905 BP; 131 A; 367 C; 298 G; 109 T; 0 U; 0 Other;

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Query Match      69.7%; Score 319.2; DB 2; Length 905;
Best Local Similarity 86.9%; Pred. No. 5.8e-49;
Matches 351; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 35 CCGGATCCAGGGCCGATGGCCAGCGCGAGCCCGGAGCCCGTCCACCCAGCGTGGG 94
Db 502 CCGCCTCCCGGGCGTCTGCGAGCCCGCGCGCGTCCGCGTCCGAGCCAGCGTGGG 561
QY 95 AGCAGTGAACCGATCCAGGAGGCGCGAGGCTCTCAACCTCTCCCGCGACACCGCG 154
Db 562 AGCAGTGAACCGATCCAGGAGGCGCGCGTCTCAACCTCTCCCGCGACACCGCG 621
QY 155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCCGATCTCCAGGAGCGACCT 214
Db 622 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCCGATCTCCAGGAGCGACCT 681
QY 215 GCCTCCAGACCGCTCGAGCTGTACAAGCAGGGCTCCGCGGACCTCACCAAGCTCA 274
Db 682 GCCTCCAGACCGCTCGAGCTGTACAAGCAGGGCTCCGCGGACCTCACCAAGCTCA 741
QY 275 AGGGCCGCTCACCATGATGGGTCCCACTACAAGCAGCACTGCCACCGACCCCGGAGA 334
Db 742 AGGGCCGCTGACCATGATGGGTCCCACTACAAGCAGCACTGCCACCGACCCCGGAGA 801
QY 335 CCTCTGCGCCACCCAGATCATCATCTTCGAGCTTCAAGGAGAACTCAAGGACTTCC 394
Db 802 CGTGTGCGCCACCCAGATCATCATCTTCGAGCTTCAAGGAGAACTCAAGGACTTCC 861
QY 395 TCCTGTGATCCGTTCCGACTGCTGGAGCGCGTGCAGGAGTGA 438
Db 862 TCCTGTGATCCGTTCCGACTGCTGGAGCGCGTGCAGGAGTGA 905

RESULT 2
AAQ03220
ID AAQ03220 standard; DNA; 896 BP.
AC AAQ03220;
XX
XX
DT 12-JUL-1990 (first entry)
DE DNA fragment of pAPO-GM-CSF encodes granulocyte macrophage colony
DE stimulating factor (GM-CSF).
XX
XX KW Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; ds.
XX OS Streptomyces sp.
XX PN EP352707-A.
XX
XX 31-JAN-1990.
XX
XX 24-JUL-1989; 89EP-00113607.
XX
XX 25-JUL-1988; 88CA-00572956.
XX
XX (CANG-) CANGENE CORP.
XX
XX Garvin RT, Malek LT;
XX
XX WPI; 1990-031296/05.
XX
XX gene expression system directing secretion of protein in Streptomyces -
XX contg. structural gene, esp. for granulocyte macrophage colony
XX stimulating factor, and regulatory sequence.
XX
XX Disclosure; Fig 3; 39pp; English.
XX
XX GM-CSF, or a wide range of other proteins, is secreted in unglycosylated
XX form, with correctly positioned intramolecular disulphide bonds and full
XX biological activity. pAPO-GM-CSF contains the BamHI HindIII fragment with
XX an aminoglycoside phosphotransferase promoter and the protease B signal
XX peptide. GM-CSF is potentially useful in cancer treatment

Query Match      69.5%; Score 318.4; DB 2; Length 896;
Best Local Similarity 89.3%; Pred. No. 8.1e-49;
Matches 343; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTCGAGCAGCTGAACCGCATCCAG 114
Db 513 GCGCCCGCGCGTCCGCCCTCGCGCTCGACCCAGCCGTCGAGCAGCTGAACCGCATCCAG 572
QY 115 GAGGCGCGGAGCTCTCAACCTCTCCGCGACACCGCGCGGAGATGAACGAGACCGTG 174
Db 573 GAGGCGCGCGCTCTCAACCTCTCGCGGACACCGCGCGGAGATGAACGAGACCGTG 632
QY 175 GAGGTGATCTCCGAGATGTTCCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCCGAG 234
Db 633 GAGGTGATCTCCGAGATGTTCCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCCGAG 692
QY 235 CTGTACAAGCAGGGCTCCGCGGACGCTCAACAGCTCAAGGGCCGCTCAACCATGATG 294
Db 693 CTGTACAAGCAGGGCTCCGCGGACGCTCAACAGCTCAAGGGCCGCTCAACCATGATG 752
QY 295 GCGTCCCACTACAAGCAGCACTGCCACCGACCCGCGGAGACCTCTCGCGCCACCCAGATC 354
Db 753 GCGTCCCACTACAAGCAGCACTGCCACCGACCCGCGGAGACCTCTCGCGCCACCCAGATC 812
QY 355 ATCAGCTTCGAGAGCTTCAAGGAGAACTCAAGGAGACTTCTCTCTGATCCGCTTCGAC 414
Db 813 ATCAGCTTCGAGAGCTTCAAGGAGAACTCAAGGAGACTTCTCTCTGATCCGCTTCGAC 872
QY 415 TCCTGGAGCGCGTGCAGGAGTGA 438
Db 873 TCCTGGAGCGCGTGCAGGAGTGA 896

RESULT 3
AAQ03219
ID AAQ03219 standard; DNA; 386 BP.
AC AAQ03219;
XX
XX
DT 12-JUL-1990 (first entry)
DE DNA fragment encodes granulocyte macrophage colony stimulating factor (GM
DE -CSF).
XX
XX KW Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; ds.
XX OS Streptomyces sp.
XX PN EP352707-A.
XX
XX 31-JAN-1990.
XX
XX 24-JUL-1989; 89EP-00113607.
XX
XX 25-JUL-1988; 88CA-00572956.
XX
XX (CANG-) CANGENE CORP.
XX
XX Garvin RT, Malek LT;
XX
XX WPI; 1990-031296/05.
XX
XX gene expression system directing secretion of protein in Streptomyces -
XX contg. structural gene, esp. for granulocyte macrophage colony
XX stimulating factor, and regulatory sequence.
XX
XX Claim 4; Fig 1; 39pp; English.
XX
XX GM-CSF, or a wide range of other proteins, is secreted in unglycosylated
XX form, with correctly positioned intramolecular disulphide bonds and full
```


CC biological activity. GM-CSF is potentially useful in cancer treatment
XX Sequence 386 BP; 73 A; 141 C; 116 G; 56 T; 0 U; 0 Other;
SQ Query Match 68.8%; Score 315; DB 2; Length 386;
Best Local Similarity 91.7%; Pred. No. 3.4e-48;
Matches 333; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 76 CCGTCACCCAGCCGCTGGAGACACGTAAGCGGATCCAGAGGCCCGCAGGCTCTCAAC 135
DB 24 CCGTCACCCAGCCGCTGGAGACACGTAAGCGGATCCAGAGGCCCGCAGGCTCTCAAC 83
QY 136 CTCTCCCGGACACCCCGCCGAGATGACGAGACCGTGGAGTGATCTCCGAGATGTC 195
DB 84 CTCTCCCGGACACCCCGCCGAGATGACGAGACCGTGGAGTGATCTCCGAGATGTC 143
QY 196 GATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGCTGTACAAGCAGGCGCTCCGC 255
DB 144 GACTTCAGGAGCCAGCTGCTCCAGACCCGCTCGAGCTGTACAAGCAGGCGCTCCGC 203
QY 256 GGCAGCCTCACCAAGCTCAAGGCCCGCTCACCATGATGCGTCCCACTACAAGCAGCAC 315
DB 204 GGCAGCCTCACCAAGCTCAAGGCCCGCTCACCATGATGCGTCCCACTACAAGCAGCAC 263
QY 316 TGCCACCCAGCCCGGAGACCTCTCGGACCCAGATCATCATCTTCGAGCTTCAAG 375
DB 264 TGCCACCCAGCCCGGAGACCTCTCGGACCCAGATCATCATCTTCGAGCTTCAAG 323
QY 376 GAGAACTCAAGGACTTCCTCTCGTGTATCCCGTTCGACTGCTGGAGCGGTGCAGGAG 435
DB 324 GAGAACTCAAGGACTTCCTCTCGTGTATCCCGTTCGACTGCTGGAGCGGTGCAGGAG 383
QY 436 TGA 438
DB 384 TGA 386
RESULT 4
AD120788
ID AD120788 standard; DNA; 435 BP.
XX AC AD120788;
XX DT 22-APR-2004 (first entry)
XX DE Human GM-CSF associated DNA #1.
XX OS mammalian granulocyte macrophage-colony stimulating factor; GM-CSF;
XX KW immunostimulant; Cytostatic; vaccine; ds.
XX OS Homo sapiens.
XX PN WO2004004742-A1.
XX PD 15-JAN-2004.
XX PF 03-JUL-2003; 2003WO-US020908.
XX PR 03-JUL-2002; 2002US-00188056.
XX PA (VAXI-) VAXIM INC.
XX PI Qiu J, Lai W, Chu YL, Li FQ;
XX WP1; 2004-099342/10.
XX DR New DNA sequence comprising a codon optimized sequence encoding a
XX PT mammalian granulocyte macrophage-colony stimulating factor, useful as an
XX PT adjuvant for enhancing an immune response of a mammal to preventive or
XX PT therapeutic vaccine.
XX PS Disclosure; SEQ ID NO 31; 42pp; English.
XX

CC The present invention relates to a DNA sequence comprising a codon-
CC optimized sequence encoding a mammalian granulocyte macrophage-colony
CC stimulating factor (GM-CSF), is new, where the codon optimized sequence
CC is different from the corresponding wild type GM-CSF encoding DNA, where
CC a codon in the codon optimized sequence has been altered to enhance the
CC expression of the mammalian GM-CSF. The method is useful as an adjuvant
CC in gene therapy or in vaccination for enhancing an immune response of a
CC mammal to a preventive or therapeutic vaccine, is also useful for
CC treating cancer or for effecting gene therapy. Use of the DNA sequence
CC comprising a codon optimized sequence encoding a mammalian granulocyte
CC macrophage-colony stimulating factor as an adjuvant results in improved
CC adjuvant activity when expressed in vivo compared with the native GM-CSF
CC gene sequence. The present sequence represents human GM-CSF associated
CC encoding sequence.
XX
SQ Sequence 435 BP; 94 A; 151 C; 128 G; 62 T; 0 U; 0 Other;
Query Match 68.3%; Score 312.6; DB 12; Length 435;
Best Local Similarity 82.8%; Pred. No. 9.3e-48;
Matches 357; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 8 GGATGCACCCACCCACCCACCTCTCCGCGCATCGAGGCGCGCATGGCGCCAGCGCGCA 67
DB 5 GGCTGCAGAGCCTGCTCTCTGCTGGGCACCGTGGCTGCAGCATCAGCGCTCCCGCCAGAA 64
QY 68 GCCGAGCCCGTCCACCCAGCCGCTGGAGACGCTGAACCGGATCCAGGAGGCCCGCAGGC 127
DB 65 GCCCAGCCCGCTCCACCCAGCCCTGGAGACGCTGAACCGCATCCAGGAGGCCAGACGGC 124
QY 128 TCTCAACCTCTCCCGGACACCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
DB 125 TGTGAACCTGTCCAGAGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184
QY 188 AGATGTTGATCTCCAGAGCCGACCTGCTCTCAGACCCGCTCGAGCTGTACAAGCAGG 247
DB 185 AGATGTTGATCTCCAGAGCCGACCTGCTCTCAGACCCGCTCGAGCTGTACAAGCAGG 244
QY 248 GCTTCGCGGCGAGCTTCAACAGCTCAAGGCGCCGCTCAACATGATGGCGTCCACTTACA 307
DB 245 GACTCGGGGAGCCTGACCAAGCTGAAGGAGCCCTGACCATGATGGCGAGCCTACTACA 304
QY 308 AGCAGCAGTCCCGACCCGAGACCTCTCTCGGCGACCCAGATCATCATCTTCGAGA 367
DB 305 AGCAGCAGTCCCGTCCCGACCCGAGACCGAGTGGCGCCACCCAGATCATCATCTTCGAGA 364
QY 368 GCTTCAAGGAGAACCTCAAGGACTTCTCTCTGATCCGTTCCGACTGCTGGAGCGCG 427
DB 365 GCTTCAAGGAGAACCTGAAGGACTTCTCTCTGATCCGTTCCGACTGCTGGAGCGCG 424
QY 428 TGCAGGAGTGA 438
DB 425 TGCAGGAGTGA 435
RESULT 5
AD120790
ID AD120790 standard; DNA; 435 BP.
XX AC AD120790;
XX DT 22-APR-2004 (first entry)
XX DE Human GM-CSF associated DNA #3.
XX KW mammalian granulocyte macrophage-colony stimulating factor; GM-CSF;
XX OS immunostimulant; Cytostatic; vaccine; ds.
XX PN Homo sapiens.
XX PD WO2004004742-A1.
XX PS 15-JAN-2004.
XX

Db 352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCTCTGCTGCTGATCCCTTCGAT 411
 QY 415 TGCTGGAGCCGCTGCAGAGT 436
 Db 412 TGCTGGAGCCGCTGCAGAGT 433

RESULT 7
 AAQ97169
 ID AAQ97169 standard; DNA; 777 BP.
 XX
 AC AAQ97169;
 DT 25-AUG-1999 (first entry)
 XX
 DE pMON13022 DNA encoding IL-3 fusion protein.
 XX
 KW Interleukin-3; CSF; colony stimulating factor; cytokine; lymphokine;
 KW mutant; mutagen; fusion protein; linker; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09521254-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 02-FEB-1995; 95WO-US001185.
 XX
 PR 04-FEB-1994; 94US-00192325.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;
 XX
 DR WPI: 1995-283774/37.
 DR P-PSDB; AAR79317.
 XX
 XX Fusion proteins comprising a human interleukin-3 variant, a linker and
 PT interleukin-3, a variant or a colony stimulating factor - useful to
 PT increase haematopoietic cell prodn. in a mammal.
 XX
 PS Claim 22; Page 158-159; 447pp; English.

A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
 R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
 interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
 including cytokine, lymphokine, interleukin, haematopoietic growth factor
 or IL-3 variant, and L is a linker. Generic sequences are described in
 CC AAW03235 - AAW03242, and specifically claimed examples are shown in
 CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
 CC recombinant DNA techniques. Specifically claimed examples of DNA
 CC sequences (including the present sequence) which encode these proteins
 CC are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
 CC used to increase haematopoietic cell production. It is also useful as an
 CC IL-3 antagonist or as a discrete antigenic fragment for production of
 CC antibodies useful in immunoassays and immunotherapy. Antagonists are used
 CC to block the growth of certain cancer cells and in treatment of asthma.
 CC The fusion protein can also be used to stimulate bone marrow and blood
 CC cell activation and growth in vitro before infusion; and to treat
 CC diseases characterised by decreased levels of myeloid, erythroid,
 CC lymphoid and/or megakaryocyte cells of the haematopoietic system. The
 CC protein has the usual activity of both its component proteins, but may
 CC have increased synergistic activity and reduced undesired side effects

Query Match 61.9%; Score 283.6; DB 2; Length 777;
 Best Local Similarity 81.6%; Pred. No. 1.6e-42;
 Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
 QY 34 TCCGGCATCGAGGGCCGCAATGGCGCCAGCGCGAGCCGCGTCCACCCAGCGGTGG 93

Db 376 TCTGGCGGCGGCTCAACATGGACCGGCTCGTTCCCGCTCCCGTCTACCCAGCGTGG 435
 QY 94 GAGCAGCTGAACGCGGATCCAGGAGGCCCGCAGGCTCTCTCAACCTCTCCCGCGACCGCC 153
 Db 436 GAAACAGCTGAATGCCATCCAGGAGGCCCGCGGCTCTCTGAACCTGAGTAGAGACACTGCT 495
 QY 154 GCGGAGATGAACGAGACCGCTGGAGGTGATCTCGAGATGTTGATCTCAAGGAGCGGACC 213
 Db 496 GCTGAGATGAATGAACAGTAGAAGTGATATCAGAAATGTTTGAACCTCCAGGAGCGGACT 555
 QY 214 TGCCTCCAGACCGCTCGAGCTGTACAAGCAGGCGCTCCGGGCGAGCTCTACCAAGCTC 273
 Db 556 TGCCTACAGACCGCTCGAGCTGTACAAGCAGGCGCTCCGGGCGAGCTCTACCAAGCTC 615
 QY 274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAGCTGCCACCGACCGCGGAG 333
 Db 616 AAGGGCCCGCTTGACCATGATGGCGCAGCTACAAGCAGCAGCTGCCCTCCAAACCCGGAA 675
 QY 334 ACTCTCTGCGCCACCGCAGATCATCACTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
 Db 676 ACTTCTGTGCAACCCAGATTATCACTTTGAAAGTTTCAAGAGAACCTGAAGGACTTC 735
 QY 394 CTCCTCGTATCCCGTTGACTGCTGGGAGCCGCTGCAGGAG 435
 Db 736 CTGCTGTGATCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 8
 AAA03723
 ID AAA03723 standard; DNA; 777 BP.
 XX
 AC AAA03723;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE Human interleukin-3 mutant containing fusion protein DNA SEQ ID NO:55.
 XX
 KW Human; interleukin 3; IL-3; mutant; mutagen; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;
 KW radiation therapy; chemotherapy; bone marrow suppressive drug;
 KW bone marrow activation; blood cell activation; blood transplant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US6022535-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 06-JUN-1995; 95US-00469318.
 XX
 PR 04-FEB-1994; 94US-00192325.
 PR 02-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95US-00411795.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
 PI Paik K, Thomas JW, McKearn JP, Olins PO, Caparon MH;
 XX
 DR WPI: 2000-160368/14.
 XX
 XX Treating hematopoietic disorders with fusion proteins comprising mutated
 PT interleukin-3 fused with secondary colony stimulating factors or other
 PT interleukin-3 variants.
 XX
 PS Example 27; Col 135-136; 276pp; English.
 XX
 CC Methods have been developed for treating haematopoietic disorders with
 CC fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
 CC 3) variants or mutant proteins (mutagens) fused with secondary colony

Db 556 TGCTACAGACCCGCTGGAGCTGTAACAGAGGCTGGGGGAGCTCACAGCTC 615
Qy 274 AAGGCGCCGCTCACCATGATGGCGTCCCACTAAGCAGCACTGCCACCAGCCCGGAG 333
Db 616 AAGGCGCCCTTGACCATGATGGCGGAGCACTAAGCAGCACTGCCCTCCAAAGCCCGAA 675
Qy 334 ACCTCTGCGCCACCCAGATCATCAGCTTCGAGAGCTTCAGGAGACCTCAAGGACTTC 393
Db 676 ACTTCTGTGCAACCCAGATTATACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTC 735
Qy 394 CTCTCTGTATCCCGTTTCGACTGTGGGAGCCGTCAGGAG 435
Db 736 CTGCTGTATCCCTTTGACTGCTGGAGCCAGTCAGGAG 777

RESULT 10

ADJ14267
ID ADJ14267 standard; DNA; 777 BP.

XX ADJ14267;

XX 20-MAY-2004 (first entry)

XX DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 55.

XX stem cell; antianaemic; immunostimulant; immunomodulator;
XX antiinflammatory; dermatological; immunosuppressive; cytostatic;
XX neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
XX lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
XX Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
XX myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.

XX Unidentified.

XX US2003185790-A1.

XX 02-OCT-2003.

XX 26-FEB-2002; 2002US-00083446.

XX 24-NOV-1992; 92US-00981044.

XX 22-NOV-1993; 93WO-US011197.

XX 04-FEB-1994; 94US-00192325.

XX 02-FEB-1995; 95WO-US001185.

XX 06-APR-1995; 95US-00411795.

XX 06-JUN-1995; 95US-00446872.

XX 09-DEC-1996; 96US-00762227.

XX (BAUE/) BAUER S C.

XX (ABRA/) ABRAMS M A.

XX (BRA/) BRAFORD-GOLDBERG S R.

XX (CAPA/) CAPARON M H.

XX (EAST/) EASTON A M.

XX (KLEI/) KLEIN B K.

XX (MCKE/) MCKEARN J P.

XX (OLIN/) OLINS P O.

XX (PAIK/) PAIK K.

XX (THOM/) THOMAS J W.

XX Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;

XX Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;

XX WPI; 2004-096775/10.

CC chimera protein, followed by harvesting of the cultured stem cells. The
CC method of the invention has antianaemic, immunostimulant, the
CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC cytostatic and neuroprotective applications and may be useful to target
CC haemopoietic cells for gene therapy, preferably for treating patients
CC having a haemopoietic disorder characterised by decreased levels of
CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC system. The expanded ex vivo cells may be used to treat neutropenia,
CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC myelofibrosis. The current sequence is that of a DNA related to the human
CC interleukin-3 (IL-3) mutant protein of the invention.

XX Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Query Match 61.9%; Score 283.6; DB 12; Length 777;

Best Local Similarity 81.6%; Pred. NO. 1.6e-42;

Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 34 TCGGCGATCGAGGCGCGATGGCGCGCAGCGCGAGCCCGGCGCTCCACCGAGCGGTGG 93

Db 376 TCTGGCGCGGCTCCAAACATGGCACCGGCTGTTCCCGCTTACCCAGCGGTGG 435

Qy 94 GAGCAGGTGAACGCGATCCAGGAGGCCCGCAGGCTCTCAACCTCTCCCGCGACACCGCC 153

Db 436 GAACAGTGAATGCCATCCAGGAGGCCCGGCGTCTCTGAACCTGAGTAGAGACTGCT 495

Qy 154 GCCGAGATGAACGAGACCGGTGGAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCGGACC 213

Db 496 GCTGAGATGATGAACAGTAGAAGTATATCAGAAATGTTTGACCTCCAGGAGCGGACT 555

Qy 214 TGCTCCAGACCGCGCTCGAGCTGTACAAGAGGGGCTCCGCGGAGCTTCACAGAGCTC 273

Db 556 TGCTACAGACCGCGCTGGAGCTGTACAAGAGCGGGCTTCGCGGGGAGCTTCACCAAGCTC 615

Qy 274 AAGGCGCGCTCACCATGATGGCGTCCCACTACAAGCAGCAGCTCCACCGAGCGGAG 333

Db 616 AAGGCGCGCTTGACCATGATGGCGGAGCTTCAAGCAGCAGCTGCGCTCCAAAGCGGAA 675

Qy 334 ACCTCTGCGGCCACCCAGATCATCATCTTCGAGAGCTTCAAGGAGAACTTCAAGGACTTC 393

Db 676 ACTTCTGTGCAACCCAGATTAATCACCCTTGAAGTTTCAAGAGAACTTGAAGGACTTC 735

Qy 394 CTCCTCGTATCCCGTTTCGACTGCTGGAGCCGCTGAGGAG 435

Db 736 CTGCTTGTATCCCTTTGACTGCTGGAGCCAGTCAGGAG 777

RESULT 11

AAQ97208

ID AAQ97208 standard; DNA; 402 BP.

XX AC AAQ97208;

XX 25-AUG-1999 (first entry)

XX pMON13012 DNA sequence.

XX Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
XX mutant; mutein; fusion protein; linker; ss.

XX Synthetic.

XX OS Homo sapiens.

XX PN WO9521254-A1.

XX PD 10-AUG-1995.

XX PF 02-FEB-1995; 95WO-US001185.

XX PR 04-FEB-1994; 94US-00192325.

XX (SEAR) SEARLE & CO G D.

Qy	172	GTGAGGTTGATCTCCGAGATGTTTCGATCTTCAGAGCGGACCTGCCTCTCAGACCCGCTC	231
Db	121	GTAGAAGTGATATCATGAAATGTTTGACCTCCAGGAGCCGACTTGCCTTCAGAGACCCGCTG	180
Qy	232	GAGCTGTACAAGCAGGGGCTCCGGCGGAGCCTCACCAGGCTCAAGGGCCGCTCACCATG	291
Db	181	GAGCTGTACAGCAGGGGCTCCGGGGGAGCCTCACCAGGCTCAAGGGCCCTTGACCATG	240
Qy	292	ATGGCGTCCCCACTACAAGCAGCACTGCCACCGACCCCGAGACCTCTCGCGCACCCAG	351
Db	241	ATGGCCAGCCACTACAAGCAGCACTGGCCCTCCAAACCCCGGAAACTTCTGTGCAACCCAG	300
Qy	352	ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCTCTCTCGTGATCCCGTTC	411
Db	301	ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGTGTTGTCATCCCTTT	360
Qy	412	GACTCTGGGAGCGGTGCAGGAGTGA	438
Db	361	GACTCTGGGAGCCAGTCCAGGAGTGA	387
RESULT 13			
ABX00086			
ID	ABX00086 standard; DNA; 402 BP.		
XX			
AC	ABX00086;		
XX			
DT	18-DEC-2002 (first entry)		
DE	Human interleukin-3 associated DNA sequence #77.		
XX			
KW	Haematopoietic factor; GM-CSF; colony stimulating factor; CSP-1; ds;		
KW	G-CSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;		
KW	human growth hormone; B-cell growth factor; leukaemia;		
KW	B-cell differentiation factor; eosinophil differentiation factor;		
KW	stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;		
KW	thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;		
KW	systemic lupus erythematosus; SLE; myelodysplastic syndrome;		
XX	myelofibrosis; Interleukin-3; IL-3; stem cell.		
OS	Unidentified.		
XX			
PN	US6436387-B1.		
XX			
PD	20-AUG-2002.		
XX			
XX	09-DEC-1996; 96US-00762227.		
XX			
PR	24-NOV-1992; 92US-00981044.		
PR	22-NOV-1993; 93WO-US011197.		
PR	04-FEB-1994; 94US-00192335.		
PR	04-FEB-1995; 95WO-US001185.		
PR	06-APR-1995; 95US-00411795.		
PR	06-JUN-1995; 95US-00446872.		

(SEAR) SEARLE & CO G D.

Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI PI
PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;

XX
DR WPI: 2002-749206/81.

Ex vivo expansion of stem cells, for enhancing transduction efficiency of cultured stem cells, comprises culturing stem cells in growth medium having mutant interleukin-3, and hematopoietic factor, and harvesting cultured cells.

XX PS Disclosure; Col 299-300; 203pp; English.

xx CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a

mutated human interleukin-3 (IL-3) sequence coupled to a haematopoietic factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-CSF γ , c-mpl ligand TPO, MGF6, erythropoietin, IL-1-13, IL-15, IL-16, flt3 ligand, human growth hormone, B-cell growth factor, B-cell differentiation factor, eosinophil differentiation factor and stem cell factor (SCF)) via a peptide linker. The formula for the chimera is given in the specification. Also included is a method for enhancing the efficiency of the transduction of cultured stem cells by a heterologous gene, comprising: (a) removing stem cells from a patient or donor; (b) culturing the stem cells with a growth medium comprising the chimera (c) transducing DNA into cultured cells; and (d) harvesting the transduced cells. The method is useful for ex vivo expansion of stem cells, and enhancing the efficiency of the transduction of cultured stem cells by a heterologous gene. The method is also useful for treating a patient having a haematopoietic disorder. The expanded haematopoietic cells are also useful in the treatment of cyclic neutropenia, aplastic anaemia, thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome, systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome and myelofibrosis. The present sequence is an IL-3 mutant associated DNA sequence. Note: The present sequence is included in the sequence listing but is not mentioned anywhere else in the specification

Query Match	61.8%;	Score 283;	DB 6;	Length 402;
Best Local Similarity	83.2%;	Pred. No. 2.1e-42;		
Matches 322;	Conservative	0;	Mismatches 65;	Indels 0;
Gaps 0				

52	ATGGCGCAGCGCGCAGCCGAGCCCGTCCACCCAGCGGTGGAGCAGTGAACGCGATC	111
1	ATGGCACCGGCTGTTCCCGCGTCCCGCTTACCCAGCGGTGGGAACACGTGAATGCCATC	60
112	CAGGAGGCCGCGAGGCTCCTCAACCTCTCCGCGACACCGCGCGGAGATGAACGAGACC	171
61	CAGGAGGCCGCGGCTCTCTCTGAACCTGAGTAGACACACTGCTGCTGAGATGAATGAACA	120
172	GTGGAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCGCTC	231
121	GTAGAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCTTACAGACCCGCGCTG	180
232	GAGCTGTCAAGCAGGGGCTTCGCGGCGAGCGCTCAACAAAGTCAAGGGCCGCTCACCATG	291
181	GAGCTGTCAAGCAGGGGCTTCGCGGGCAGCGCTCAACAAAGTCAAGGGGCCCTTGACCATG	240
292	ATGGCGTCCACTACAAAGCAGACACTGCCACCGACCCCGGAGACCTCCTGCGCCACCCAG	351
241	ATGGCAGCCACCTACAAAGCAGCACTGCCCTTCAAACCCCGGAACCTTCTGTGTGAACCCAG	300
352	ATCATCACCTTCGAGAGCTTTCAAAGGAAACCTCAAGGACTTTCCTCCTCGTGATCCCGTTC	411
301	ATTATCACCTTTGAAAGTTTCAAAGAAACCTGAAGGACTTCCTGCTGTGCATCCCCTTT	360
412	GACTGCTGGAGCGGTGACGAGTGA	438
361	GACTGCTGGAGCGCAGTCCAGGAGTGA	387

RESULT 14

RESUL 14
ADJ14388
ID ADJ14388 standard; DNA; 402 BP.

XX
AC ADJ14388;XX
DT 20-MAY-2004 (first entry)

XX
DE DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 151:

stem cell: antianaemic: immunostimulant: immunomodulator:

KW antiinflammatory; dermatological; immunosuppressive; cytostatic; stem cell; antianaemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;

KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid; lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;

KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia

KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.

[illegible]

XX OS Unidentified.
XX PN US2003185790-A1.
XX PD 02-OCT-2003.
XX XX
PF 26-FEB-2002; 2002US-00083446.
XX 24-NOV-1992; 92US-00981044.
XX 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US0001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
PR 09-DEC-1996; 96US-00762227.
XX (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAE/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX Baur SC, Abrams MA, Brafard-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;
XX WPI; 2004-096775/10.
XX Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT aplastic anemia, involves culturing the stem cells with growth medium
PT comprising chimera protein, and harvesting the cultured stem cells.
XX Disclosure; SEQ ID NO 176; 202pp; English.
XX The invention relates to a novel method whereby stem cells are ex vivo
CC expanded via culturing the stem cells with a growth medium comprising a
CC chimera protein, followed by harvesting of the cultured stem cells. The
CC method of the invention has antianemic, immunostimulant,
CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC cytostatic and neuroprotective applications and may be useful to target
CC hematopoietic cells for gene therapy, preferably for treating patients
CC having a haemopoietic disorder characterised by decreased levels of
CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC system. The expanded ex vivo cells may be used to treat neutropenia,
CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC myelofibrosis. The current sequence is that of a DNA related to the human
CC interleukin-3 (IL-3) mutant protein of the invention.
XX Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
S2 Query Match 61.8%; Score 283; DB 12; Length 402;
Best Local Similarity 83.2%; Pred. No. 2.1e-42;
Matches 322; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 52 ATGGCGCCGAGCGGAGCGGAGCGCGTCCACCCAGCCGTGGAGACGTCGACCGGATC 111
DB 1 ATGGCACCGGCTGTTCCCGCTCCCGCTACCCAGCCGTGGGAAACACGTAATGCATC 60
QY 112 CAGGAGCGCGGAGGCTCTCAACTCTCCCGGACACCGCGCGAGATGAACGAC 171
DB 61 CAGGAGCGCGGCGTCTCTTGAACTAGTAGACACACTGCTCTGAGATGAATGAACA 120
QY 172 GTGGAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTTC 231
DB 121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGAGCCGACTTGCTACAGACCCGCTG 180
QY 232 GAGCTGTACAGGAGGCGCTCCGCGGACGCTCACCAGCTCAAGGGCGGCTCACCATG 291

DB 181 GAGCTGTACAGCAGGGGCTCGGGGAGCGCTCACCAAGCTCAAGGGGCGCTTGACCATG 240
QY 292 ATGGCGTCCACTACAAGCAGCACTGCCACCGAGCCCGGAGACCTCTCTGCCGCCACCCAG 351
DB 241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCAACCCCGGAAACTTCTGTGCAACCCAG 300
QY 352 ATCATCACCTTCGAGAGCTTCAAGGAGAACTCAAGGACTTCTCTCTCGTATCCGTTTC 411
DB 301 ATTATCACCTTTGAAAGTTTCAAGAGAACTTCAAGGAGAACTTCTCTGTGTCATCCCTTT 360
QY 412 GACTCTGGGAGCCGTCGAGGAGTGA 438
DB 361 GACTCTGGGAGCCAGTCCAGGAGTGA 387
RESULT 15
AAQ97183
ID AAQ97183 standard; DNA; 822 BP.
XX AAQ97183;
XX 25-AUG-1999 (first entry)
XX PMON13035 DNA encoding IL-3 fusion protein.
XX Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.
XX Synthetic.
XX Homo sapiens.
XX WO9521254-A1.
XX 10-AUG-1995.
XX 02-FEB-1995; 95WO-US001185.
XX 04-FEB-1994; 94US-00192325.
XX (SEAR) SEARLE & CO G D.
XX Baur CS, Abrams MA, Brafard-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;
XX WPI; 1995-283774/37.
XX P-PSDB; AAR79320.
XX Fusion proteins comprising a human interleukin-3 variant, a linker and
PT interleukin-3, a variant or a colony stimulating factor - useful to
PT increase haematopoietic cell prodn. in a mammal.
XX Claim 22; Page 167-168; 447pp; English.
XX A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC or IL-3 variant, and L is a linker. Generic sequences are described in
CC AAR03235 AAR03242, and specifically claimed examples are shown in
CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC recombinant DNA techniques. Specifically claimed examples of DNA
CC sequences (including the present sequence) which encode these proteins
CC are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
CC used to increase haematopoietic cell production. It is also useful as an
CC IL-3 antagonist or as a discrete antigenic fragment for production of
CC antibodies useful in immunoassays and immunotherapy. Antagonists are used
CC to block the growth of certain cancer cells and in treatment of asthma.
CC The fusion protein can also be used to stimulate bone marrow and blood
CC cell activation and growth in vitro before infusion; and to treat
CC diseases characterised by decreased levels of myeloid, erythroid,
CC lymphoid and/or megakaryocyte cells of the haematopoietic system. The
CC protein has the usual activity of both its component proteins, but may

CC have increased synergistic activity and reduced undesired side effects

```
XX
SQ Sequence 822 BP; 222 A; 244 C; 180 G; 176 T; 0 U; 0 Other;

Query Match      61.4%; Score 281; DB 2; Length 822;
Best Local Similarity 83.1%; Pred. NO. 4.8e-42;
Matches 320; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 51 CATGGCGCCAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAT 110
Db ||||| || || || || || || || || || || || || || || || || || ||
438 CATGGCACCGGCTCGTTCCCGCTCCCGCTTACCCAGCGGTGGGAACACGTGAATGCCAT 497
QY 111 CCAGGAGGCGCGGAGCGCTCTCAACCTCTCCCGGACACCGCGCGGAGATGAACGAGAC 170
Db ||||| || || || || || || || || || || || || || || || || || ||
498 CCAGGAGGCGCGGCGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAC 557
QY 171 CGTGGAGGTGATCTCCGAGATGTTTCGATCTCCAGGAGCGGACCTGCTCCAGACCGGCT 230
Db || || || || || || || || || || || || || || || || || || || ||
558 AGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCGGACTTGCTACAGACCGGCT 617
QY 231 CGAGCTGTACAGCAGGGGCTCCGGGCGAGCTCAGCAAGCTCAAGGGCGCGCTCAACAT 290
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 GGAGCTGTACAGCAGGGGCTCCGGGCGAGCTCAGCAAGCTCAAGGGCGCGCTTGACCAT 677
QY 291 GATGGCGTCCCACTACAAGCAGCACTGCCACCGGAGCGGAGCGGAGCGGAGCGGAG 350
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
678 GATGGCGAGCCACTACAAGCAGCACTGCCCTCAACCGGAGAACTTCCTGTGCAACCCA 737
QY 351 GATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGAGCTTCCTCTGATCCCGTT 410
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
738 GATTATCACCTTTGAAAGTTTCAAGAGAACCTGAGAGACTTCCTGCTGTCATCCCTT 797
QY 411 CGACTGCTGGGAGCGGTCAGGAG 435
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
798 TGAAGCTGGGAGCCAGTCCAGGAG 822
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Search completed: March 11, 2005, 15:58:59
Job time : 425 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2005, 16:42:11 ; Search time 453 Seconds
(without alignments)
6014.183 Million cell updates/sec

Title: us-10-723-083-1

Perfect score: 458

Sequence: 1 cggccggatgcaccacca.....gtacgtcgacgcatgccc 458

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	458	100.0	458	19	US-10-723-083-1
2	318.6	69.6	429	19	US-10-723-083-3
3	312.6	68.3	435	17	US-10-188-056-31
4	311	67.9	435	17	US-10-188-056-33
5	283.6	61.9	777	16	US-10-083-446-55
6	283	61.8	402	16	US-10-083-446-176
7	281	61.4	822	16	US-10-083-446-69
8	281	61.4	903	16	US-10-083-446-66
9	277	60.5	2211	17	US-10-609-346-9
10	276.8	60.4	448	17	US-10-609-346-19
11	276.8	60.4	781	17	US-10-447-315-20
					Sequence 1, Appl
					Sequence 3, Appl
					Sequence 31, Appl
					Sequence 33, Appl
					Sequence 55, Appl
					Sequence 176, Appl
					Sequence 69, Appl
					Sequence 66, Appl
					Sequence 9, Appl
					Sequence 19, Appl
					Sequence 20, Appl

12	276.8	60.4	789	16	US-10-131-985-16	Sequence 16, Appl
13	276.8	60.4	789	19	US-10-901-417-16	Sequence 16, Appl
14	276.2	60.3	1011	13	US-10-044-090-509	Sequence 509, Appl
15	275.8	60.2	435	9	US-09-826-025-8	Sequence 8, Appl
16	275.8	60.2	435	14	US-10-083-590-14	Sequence 14, Appl
17	275.8	60.2	435	17	US-10-411-037-17	Sequence 17, Appl
18	275.8	60.2	435	17	US-10-411-026-17	Sequence 17, Appl
19	275.8	60.2	435	17	US-10-410-962-17	Sequence 17, Appl
20	275.8	60.2	435	17	US-10-411-049-17	Sequence 17, Appl
21	275.8	60.2	435	18	US-10-410-930-17	Sequence 17, Appl
22	275.8	60.2	435	18	US-10-410-997-17	Sequence 17, Appl
23	275.8	60.2	435	18	US-10-411-012-17	Sequence 17, Appl
24	275.8	60.2	435	18	US-10-287-994-17	Sequence 17, Appl
25	275.8	60.2	435	18	US-10-410-913-17	Sequence 17, Appl
26	275.8	60.2	435	18	US-10-785-577-8	Sequence 8, Appl
27	275.8	60.2	435	19	US-10-410-980-17	Sequence 17, Appl
28	275.2	60.1	505	18	US-10-688-845-82	Sequence 82, Appl
29	275.2	60.1	737	15	US-10-081-969-19	Sequence 19, Appl
30	275.2	60.1	756	15	US-10-177-390-21	Sequence 21, Appl
31	275.2	60.1	756	17	US-10-351-157-180	Sequence 180, Appl
32	275.2	60.1	756	17	US-10-352-554-165	Sequence 165, Appl
33	275.2	60.1	756	17	US-10-429-802-32	Sequence 32, Appl
34	275.2	60.1	756	17	US-10-430-503-23	Sequence 23, Appl
35	275.2	60.1	756	17	US-10-305-720-1195	Sequence 1195, Appl
36	275.2	60.1	756	18	US-10-475-024-7	Sequence 7, Appl
37	275.2	60.1	756	18	US-10-475-024-8	Sequence 8, Appl
38	275.2	60.1	767	18	US-10-666-122-4	Sequence 4, Appl
39	275.2	60.1	767	18	US-10-666-122-6	Sequence 6, Appl
40	275.2	60.1	767	19	US-10-278-698-30	Sequence 30, Appl
41	275.2	60.1	767	19	US-10-278-698-30	Sequence 30, Appl
42	275.2	60.1	1318	14	US-10-228-811-3	Sequence 3, Appl
43	274.8	60.0	579	17	US-10-449-831A-187	Sequence 187, Appl
44	274.2	59.9	435	17	US-10-188-056-32	Sequence 32, Appl
45	274.2	59.9	496	16	US-10-267-384-131	Sequence 131, Appl

ALIGNMENTS

RESULT 1

US-10-723-083-1
; Sequence 1, Application US/10723083
; Publication No. US2005050602A1
; GENERAL INFORMATION:
; APPLICANT: Altosar, Ilmar
; APPLICANT: Sardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Ganz, Peter
; APPLICANT: Tackaberry, Elleen
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: 08-898901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(438)
; OTHER INFORMATION:
US-10-723-083-1

Query Match 100.0%; Score 458; DB 19; Length 458;

Best Local Similarity 100.0%; Pred. No. 7.2e-110;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGGATGCACCACACACACACTCTCCGGCATCGAGGCGCGATGGCCCA 60

Db 1 CGGCCGGGATGCACCAACACCAACCACCTCTCTCGGGATCGAGGGCGCATGGCGCA 60
QY 61 GCGCGAGCCCGAGCCCGTCCACCCAGCCGCTGGAGACAGTGAACCGCATCCAGAGGCC 120
Db 61 GCGCGAGCCCGAGCCCGTCCACCCAGCCGCTGGAGACAGTGAACCGCATCCAGAGGCC 120
QY 121 CGCAGCTCTCAACCTCTCCCGGACACCGCCGCGGAGATGAACAGACCGTGGAGGTG 180
Db 121 CGCAGGCTCTCAACCTCTCCCGGACACCGCCGCGGAGATGAACAGACCGTGGAGGTG 180
QY 181 ATCTCCGAGATGTTGATCTCCAGGAGCGAGCTGCTCCAGACCGCTCCAGAGCTGTAC 240
Db 181 ATCTCCGAGATGTTGATCTCCAGGAGCGAGCTGCTCCAGACCGCTCCAGAGCTGTAC 240
QY 241 AGCAGGGCTCCGCGGAGCTTCAACAGCTCACCAGCTCAAGGGCCGCTCACCATGATGGGTCC 300
Db 241 AGCAGGGCTCCGCGGAGCTTCAACAGCTCACCAGCTCAAGGGCCGCTCACCATGATGGGTCC 300
QY 301 CACTACAGGAGCTGCGCCAGCGACCGCCGCGGAGACCTCTCGGCCACCCAGATCATCAC 360
Db 301 CACTACAGGAGCTGCGCCAGCGACCGCCGCGGAGACCTCTCGGCCACCCAGATCATCAC 360
QY 361 TTCGAGAGCTTCAAGGAGACCTCAAGGACTTCTCTCTGATCCGTTTCGACTGCTGG 420
Db 361 TTCGAGAGCTTCAAGGAGACCTCAAGGACTTCTCTCTGATCCGTTTCGACTGCTGG 420
QY 421 GAGCCGGTGCAGGAGTGAAGTACGCTAGCGTGCAGCGATGCCG 458
Db 421 GAGCCGGTGCAGGAGTGAAGTACGCTAGCGTGCAGCGATGCCG 458

RESULT 2

US-10-723-083-3
; Sequence 3, Application US/10723083
; Publication No. US2005005062A1
; GENERAL INFORMATION:
; APPLICANT: Alcosaar, Illimar
; APPLICANT: Sardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Ganz, Peter
; APPLICANT: Tackaberry, Eileen
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: 08-698901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
; OTHER INFORMATION:
US-10-723-083-3

Query Match 59.6%; Score 318.6; DB 19; Length 429;
Best Local Similarity 83.9%; Pred. No. 1.6e-73;
Matches 360; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 10 ATGCACACACCAACCACTCTCTCGGATCGAGGGCGGATGGCGCGAGCGCGCAGC 69
Db 1 ATGCACACACCAACCACTCTCTCGGATCGAGGGCGGATGGCGCGAGCGCGCAGC 60
QY 70 CCGAGCCCGTCCACCCAGCCGTTGGAGACGTGAACCGCATCAGAGGCCCGCAGGCTC 129
Db 61 CCAGGCCCGCAGCAGCGCCCTGGAGCATGTGAATGCCATCAGAGGCCCGGCGTCTC 120
QY 130 CTCACCTCTCCGCGACACCGCCGCGGAGATGAACGAGACCGTGGAGGTATCCGAG 189

Db 121 CTGAACCTTGAGTAGAGACACTCTCTCTGAGATGAATGAACAGTAGAGTATATCAGAA 180
QY 190 ATGTTTCGATCTCCAGAGCCCGACCTGCTCCAGACCCGCTCGAGCTGTACAGAGGCC 249
Db 181 ATGTTTCGATCTCCAGAGCCCGACCTGCTCCAGACCCGCTCGAGCTGTACAGAGGCC 240
QY 250 CTCGCGGAGGCTCACAAGCTCAAGGGCCGCTCACCATGATGGCTCCCACTACAG 309
Db 241 CTCGCGGAGGCTCACAAGCTCAAGGGCCGCTTGAACCATGATGGCCAGCCACTACAAG 300
QY 310 CAGCACTGCCACCCAGACCCCGGAGACCTCTCTGCGCCACCCAGATCATCACCTTCAGAGC 369
Db 301 CAGCACTGCCCTCCAAACCCCGGAACTTCTCTGTGCAACCCAGATTAACCTTTGAAAGT 360
QY 370 TTCAAGAGAACTCAAGGACTTCTCTCTGATGATCCGTTTCGATGCTGGAGCCGGTG 429
Db 361 TTCAAGAGAACTCAAGGACTTCTCTCTGATGATCCGTTTCGATGCTGGAGCCAGTC 420
QY 430 CAGGAGTGA 438
Db 421 CAGGAGTGA 429

RESULT 3

US-10-188-056-31
; Sequence 31, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188,056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-31

Query Match 68.3%; Score 312.6; DB 17; Length 435;
Best Local Similarity 82.8%; Pred. No. 5.7e-72;
Matches 357; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 8 GGATGCACCAACCAACCACTCTCTCGGATCGAGGGCGGATGGCGCGAGCGCGCA 67
Db 5 GGCTGCAGAGCTGTCTCTGTGGGACCGTGGCTGCAGCATCAGCGCTCCCGCCAGAA 64
QY 68 GCGCGAGCCGTCACCCAGCGCTGGAGACAGTGAACCGCATCCAGAGGCCCGCAGGC 127
Db 65 GCGCGAGCCGTCACCCAGCGCTGGAGACAGTGAACCGCATCCAGAGGCCCGCAGGC 124
QY 128 TCCTCAACCTCTCCCGGACACCGCCGCGGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
Db 125 TGCTGAACCTGTCCAGAGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCAGG 184
QY 188 AGATGTTGATCTCAGAGCGGACCTGCTCCAGACCGCGCTCGAGCTGTACAGAGCG 247
Db 185 AGATGTTGATCTCAGAGCGGACCTGCTCTCGAGACCGCGCTGGAGGTGATGAAGCAGG 244
QY 248 GCCTCCGCGGAGCTCACCAGCTCAAGGGCCGCTCACCATGATGGCTGCCACTACA 307
Db 245 GACTCGGGGAGCTGACCAAGCTGAAGGAGACCCCTGACCATGATGGCCAGCCACTACA 304
QY 308 AGCAGCACTGCCACCCAGCCCGGAGACCTCTGCGGCCACCCAGATCATCACTTCGAGA 367
Db 305 AGCAGCACTGCCCTCCACACCCCGAGACAGCTGCGGCCACCCAGATCATCACTTCGAGA 364
QY 368 GCTTCAAGAGAACCTCAAGGACTTCTCTCTGATCCCGTTTCGACTGCTGGAGCGCG 427

Db 365 GCTTCAGGAGACCTGAAGACTTCTGCTGTGTGATCCCTTCGACTGCTGGAGCCG 424
Qy 428 TGCAGGAGTGA 438
Db 425 TGCAGGAGTGA 435

RESULT 4

US-10-188-056-33
; Sequence 33, Application US/10188056
; Publication No. US2004000934A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188,056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-33

Query Match 67.9%; Score 311; DB 17; Length 435;
Best Local Similarity 82.6%; Pred. No. 1.5e-71;
Matches 356; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Qy 8 GGATGCACCAACCAACCACTCTCTCCGGCATCGAGGGCGCGCATGGCCAGCGCGCA 67
Db 5 GGCTGCAGACCTGCTCTCTGCGCACCTGGCTGCAGCATCAGGCTCCGCCAGAA 64
Qy 68 GCCGAGCGCGTCAACCAAGCGTGGAGAGCACTGTAACGGATCCAGAGGCCCGCAGGC 127
Db 65 GCCCGAGCGCGTCAACCAAGCGTGGAGAGCACTGTAACGGATCCAGAGGCCCGCAGGC 124
Qy 128 TCTCAACCTCTCCGCGACACCGCGCGAGATGACGAGCGGTGGAGTCTCG 187
Db 125 TGTGAACCTGTTCAGAGACACCGCGCGAGATGACGAGCGGTGGAGTCTCG 184
Qy 188 AGATGTTGAGTCTCCAGAGCGACCTGCTCCAGACCCCGCTCGAGCTGTACAAGCAGG 247
Db 185 AGATGTTGAGTCTCCAGAGCGACCTGCTCCAGACCCCGCTCGAGCTGTACAAGCAGG 244
Qy 248 GCTTCGCGCGAGCTCAACAGCTCAAGGGCGCGTCAACCATGATGGGTCCCACTACA 307
Db 245 GACTGCGGGCAGCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCGCAGCACTACA 304
Qy 308 AGCAGCATCTCCACCGCGAGACCTCTGCGCGACCGCATCATCATTCTGAGA 367
Db 305 AGCAGCATCTCTCCACCGCGAGACCTCTGCGCGACCGCATCATCATTCTGAGA 364
Qy 368 GCTTCAAGAGAACCTCAAGAGCTTCTCTCTGTGATCCCGTTCGACTGCTGGAGCGG 427
Db 365 GCTTCAAGAGAACCTCAAGAGCTTCTCTCTGTGATCCCTTCGACTGCTGGAGCGCG 424
Qy 428 TGCAGGAGTGA 438
Db 425 TGCAGGAGTGA 435

RESULT 5

US-10-083-446-55
; Sequence 55, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.

Bradford-Goldberg, Sarah R.
Caparon, Mairé H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kuman
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSES: S. Christopher Bauer, Pharmacia Corporation
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/083,446
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636) 737-6257
TELEFAX: (636) 737-5452
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-083-446-55
Query Match 61.9%; Score 283.6; DB 16; Length 777;
Best Local Similarity 81.6%; Pred. No. 2e-64;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy 34 TCGGAGTCGAGGGCGCATGGCGCGCAGCGCGCGAGCCGCTCCACCCAGCGGTGG 93
Db 376 TCTGGCGGGCTCCAAACATGACCGGTCTGTTCCCGCTCCCGCTACCCAGCGGTGG 435
Qy 94 GAGCAGTGAACGCGATCCAGAGGCGCGAGGCTCTCAACCTCTCCCGCGACCGCC 153
Db 436 GAACAGTGAATGCCATCCAGGAGGCGCGCGCTCTCTGAACTAGTAGACACTGCT 495
Qy 154 GCGGATGAACGAGACCGTGGAGGTGATCTCCGATGTTGATCTCCAGGAGCGGACC 213
Db 496 GCTGATGAATGAACAGTAGAAGTATCAGAAATGTTGACTCTCAGGAGCGGACT 555
Qy 214 TGCCTCCAGACCGCTCGAGCTGTACAAGCAGGCGCTCCCGCGAGCTTCACCAAGCTC 273
Db 556 TGCTACACACCGCTCGAGCTGTACAAGCAGGCGCTCCCGCGAGCTTCACCAAGCTC 615
Qy 274 AAGGGCCCGCTCACCATGATGGCGTCCCTACTACAAGCAGACTGCCCCACCGACCGGAG 333

Db 616 AAGGGCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCGCTCCAAACCCGGAA 675
QY 334 ACCTCTGCGCCACCCAGATCATCACTTCGAGAGCTTCAAGGAGAACTCAAGGACTTC 393
Db 676 ACTTCTGTGCAACCCAGATTAATCACTTTGAAAGTTTCAAGAGAACTGAAGGACTTC 735
QY 394 CTCTCGTATCCCGTTGCACTCTGCGAGCCGGTGCAGAG 435
Db 736 CTGCTTGTATCCCTTTGACTCTGCGAGCCAGTCCAGAG 777

RESULT 6
US-10-083-446-176
; Sequence 176, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olin, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
; Corporate Patent Dept., Mail Zone 04E
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,446
; FILING DATE: 26-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/762,227
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 08/446,872
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305
; REFERENCE/DOCKET NUMBER: C-2790/6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (636)737-6257
; TELEFAX: (636)737-5452
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-10-083-446-176
Query Match 61.8%; Score 283; DB 16; Length 402;
Best Local Similarity 83.2%; Pred. No. 3e-64;

Matches 322; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 52 ATGGCGCCAGCGCGAGCCGAGCCGCTCCACCCAGCGCTGGAGCAGCTGAACGCGATC 111
Db 1 ATGGCACCAGCTCGTTCCCGCTCCCGCTTACCCAGCGTGGGAACACGTAATGCCATC 60
QY 112 CAGGAGGCGCGAGCGCTCTCAACCTCTCCCGCGACACCGCGCGAGATGAACGAGACC 171
Db 61 CAGGAGGCGCGCGCTCTCTGAACCTGAGTACAGACACTGCTGCTGAGATGAATGAACA 120
QY 172 GTGGAGGTGATCTCCGAGATGTTTCATCTCCAGGAGCGGACCTGCTCCAGACCCGCTC 231
Db 121 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGGACTTGCCTACAGACCCGCTG 180
QY 232 GAGCTGTACAAGCAGGCGCTCCCGCGAGCGCTCACAAGCTCAAGGCGCGCTCAACCATG 291
Db 181 GAGCTGTACAAGCAGGCGCTCCCGCGAGCGCTCACAAGCTCAAGGCGCGCTTGGACATG 240
QY 292 ATGGCGTCCCACTACAAGCAGCACTGCGCCACCGAGCGAGACCTCTGCGCCACCCAG 351
Db 241 ATGGCAGCGCACTACAAGCAGCACTGCGCTCCCAACCCCGGAACTTCTGTGCAACCCAG 300
QY 352 ATCATCAGCTTCGAGAGCTTCAAGGAGAACTCAAGGACTTCTCTGATCCGCTTC 411
Db 301 ATTATCAGCTTTGAAAGTTTCAAGAGAACTTCAAGGAGAACTTCTCTGCTGTCATCCCTTT 360
QY 412 GACTCTGGGAGCGCGTGCAGGAGTGA 438
Db 361 GACTCTGGGAGCGGAGTGCAGGAGTGA 387

RESULT 7
US-10-083-446-69
; Sequence 69, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olin, Peter O.
; Paik, Kuman
; Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
; Corporate Patent Dept., Mail Zone 04E
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,446
; FILING DATE: 26-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/762,227
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 08/446,872
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305
; REFERENCE/DOCKET NUMBER: C-2790/6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (636)737-6257
; TELEFAX: (636)737-5452
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-10-083-446-176
Query Match 61.8%; Score 283; DB 16; Length 402;
Best Local Similarity 83.2%; Pred. No. 3e-64;

ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-083-446-69

Query Match 61.4%; Score 281; DB 16; Length 822;
Best Local Similarity 83.1%; Pred. No. 9.7e-64;
Matches 320; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 51 CATGGCGCCAGCGCGAGCCGCGTCCACCCAGCGGTGGAGCAGTGAACCGCAT 110
DB 438 CATGGCACCGGCTCGTTCCCGTCCCGTCTACCCAGCGGTGGAGACAGTGAATGCCAT 497
QY 111 CCAGGAGGCGCGAGGCTCTCAACCTCTCCCGCGACACCGCGCGGAGATGAACGAGAC 170
DB 498 CCAGGAGGCGCGGCGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAC 557
QY 171 CGTGGAGGTGATCTCCGAGATGTTCCATCTCCAGGAGCGGACCTCCAGACCGCGCT 230
DB 558 AGTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGGACTTGCTCAGACCGCGCT 617
QY 231 CGAGCTGTACAGCAGCGGCTCCGCGGAGCGCTCCAGAGCTCAAGGCGCGCTCAACCAT 290
DB 618 GGAGCTGTACAGCAGCGGCTCCGCGGAGCGCTCCAGAGCTCAAGGCGCGCTTGACCAT 677
QY 291 GATGGCGTCCCACTACAAGCAGACACTGCCACCGACCGCGGAGACCTCTCTGTCGCGCCACCA 350
DB 678 GATGGCGGCGGCACTACAAGCAGCACTGCCCTCCAAACCGCGGAACTTCTGTGCAACCCA 737
QY 351 GATCATCACTTCGAGAGCTTCAAGAGAACCTCAAGGACTTCTCTGTCGTCGCTTCCGCTT 410
DB 738 GATTATCACTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTCTGTCGTCGCTTCCGCTT 797
QY 411 CGACTGCTGGGAGCGGTGCAGGAG 435
DB 798 TGACTGCTGGGAGCGGTGCAGGAG 822

RESULT 8
US-10-083-446-66
Sequence 66, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olines, Peter O.
Paik, Kuman
Thomas, John W.
TITLE OF INVENTION: Methods of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
STREET: 800 N. Lindbergh
CITY: St. Louis

STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-083-446-66

Query Match 61.4%; Score 281; DB 16; Length 903;
Best Local Similarity 83.1%; Pred. No. 9.7e-64;
Matches 320; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 51 CATGGCGCCAGCGCGAGCCGCGTCCACCCAGCGGTGGAGCAGTGAACCGCAT 110
DB 519 CATGGCACCGGCTCGTTCCCGTCCCGTCTACCCAGCGGTGGAGACAGTGAATGCCAT 578
QY 111 CCAGGAGGCGCGAGGCTCTCTCAACCTCTCCCGCGACACCGCGCGGAGATGAACGAGAC 170
DB 579 CCAGGAGGCGCGGCGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAC 638
QY 171 CGTGGAGGTGATCTCCGAGATGTTCCATCTCCAGGAGCGGACCTGCTCAGACCGCGCT 230
DB 639 AGTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGGACTTGCTCAGACCGCGCT 698
QY 231 CGAGCTGTACAGCAGCGGCTCCGCGGAGCGCTCCAGAGCTCAAGGCGCGCTCAACCAT 290
DB 699 GGAGCTGTACAGCAGCGGCTCCGCGGAGCGCTCCAGAGCTCAAGGCGCGCTTGACCAT 758
QY 291 GATGGCGTCCCACTACAAGCAGCACTGCCACCGACCGCGGAGACCTCTCTGCGCCACCCA 350
DB 759 GATGGCGGCGGCACTACAAGCAGCACTGCCCTCCAAACCGCGGAACTTCTGTGCAACCCA 818
QY 351 GATCATCACTTCGAGAGCTTCAAGAGAACCTCAAGGACTTCTCTGTCGTCGCTTCCGCTT 410
DB 819 GATTATCACTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTCTGTCGTCGCTTCCGCTT 878
QY 411 CGACTGCTGGGAGCGGTGCAGGAG 435
DB 879 TGACTGCTGGGAGCGGTGCAGGAG 903

RESULT 9
US-10-609-346-9
Sequence 9, Application US/10609346
Publication No. US20040063635A1

GENERAL INFORMATION:
APPLICANT: Yu, Zailin
TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLOGICAL ACTIVITY
FILE REFERENCE: ZYU-0603
CURRENT APPLICATION NUMBER: US/10/609,346
CURRENT FILING DATE: 2003-06-26
PRIOR APPLICATION NUMBER: US 60/392,948
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 2211
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA of HSA-GMCSF

US-10-609-346-9

Query Match 60.4%; Score 277; DB 17; Length 2211;
Best Local Similarity 82.0%; Pred. No. 1.1e-62;
Matches 319; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 50 GCATGGCGCCAGCGCCGAGCCCGTCCACCCAGCGCGTGGAGACGTGAACGCGA 109
DB 1823 GCTTAGCACCGCCGCTCGCCCGAGCCGAGCACGCGCCCTGGAGCATGTGAATGCCA 1882
QY 110 TCAGAGAGCCCGCAGGCTCTCAACTCTCCCGGACACCGCCGCGAGATGACGAGA 169
DB 1883 TCAGAGAGCCCGCGCTCTCTGAACTGAGTAGACACACTGCTGTGAGATGAATGAAA 1942
QY 170 CCGTGGAGGTGATCTCCGAGATCTCCGAGTCTCCAGGAGCGACCTGCTCCAGACCCGCC 229
DB 1943 CAGTAGAGTCACTCAGAAATGTTGACCTCCAGAGCGGACCTGCTTACAGACCCGCC 2002
QY 230 TCAGAGTGTAAAGAGCGGCTCCGCGGAGCTCTCAAGTCTCAAGGCGCCGCTCACCA 289
DB 2003 TGGAGCTGTACAAAGCAGGGGCTCGCGGAGCGCTCAACAGCTCAAGGCGCCCTTGACCA 2062
QY 290 TGATGGCTCCCACTACAGCAGCTGCGCCAGCGCCGAGACCTCTGCGCCACCC 349
DB 2063 TGATGGCCAGCCACTACAGCAGCTGCGCCCTCAACCCCGGAACTTCTGTGCAACCC 2122
QY 350 AGATCATCACTTCGAGAGCTTCAAGGAGAACTCAAGGACTTCTCTCTGATCCCGT 409
DB 2123 AGATTATCACTTTGAAGTTTCAAGAGAACTTCAAGGACTTCTGCTGTGATCCCT 2182
QY 410 TCAGTGTGGGAGCGGTCGAGAGTGA 438
DB 2183 TTGACTGCTGGAGCCAGTCCAGGAGTGA 2211

RESULT 10
US-10-609-346-19
; Sequence 19, Application US/10609346
; Publication No. US20040063635A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Zailin
; APPLICANT: Fu, Yan
; TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLOGICAL ACTIVITY
; FILE REFERENCE: ZYU-0603
; CURRENT APPLICATION NUMBER: US/10/609,346
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US 60/392,948
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-609-346-19

Query Match 60.4%; Score 276.8; DB 17; Length 448;
Best Local Similarity 77.5%; Pred. No. 1.2e-62;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 8 GGATGACACACACACACCACTCTCTCGGATCGAGGCGCGATGGCGCGCGCA 67
DB 5 GGCTGACAGGCTGTGCTCTTGGCACTGTGGCTGCGCATCTCTGACCCCGCGCT 64
QY 68 GCCGAGCCCGTCCACCCAGCGCTGGAGCGGTGAACGCGATCCAGGAGGCCCGCAGGC 127
DB 65 CGCCAGCCCCAGCAGCGCCCTGGAGCATGTGAATGCCATCCAGGAGGCCCGCGTC 124
QY 128 TCCTCAACCTCTCCCGCGACACCGCGCGAGATGAAGAGAGACCGTGGAGGTGATCTCG 187
DB 125 TCCTGACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCACTCAG 184
QY 188 AGATGTTGATCTCCAGGAGCGCACTGCTCTCCAGCCGCTCGAGCTGTACAGCAGG 247
DB 185 AAATGTTGACCTCCAGGAGCGCACTGCTCTACAGACCGCTGGAGCTGTACAAGCAGG 244
QY 248 GCCTCGCGGCGACCTCAACAGCTCAAGGCGCCGCTCACCATGATGGGTCCCACTACA 307
DB 245 GCCTCGGCGGAGCTCAACAGCTCAAGGCGCCCTTGACCAATGATGGCCAGCCACTACA 304
QY 308 AGCAGCACTGCCCAACCGCGAGAGCTCTCTGCGCCACCCAGATCATCACTTCGAGA 367
DB 305 AGCAGCACTGCCCTCAACCCCGGAACTTCTCTGCAACCCAGATTAATCACTTTGAA 364
QY 368 GTTCAAGGAGAACTCAAGGACTTCTCTCTGATCCCGTTCGACTGCTGGAGCGCG 427
DB 365 GTTCAAGGAGAACTCAAGGACTTCTCTCTGATCCCGTTCGACTGCTGGAGCGCG 424
QY 428 TCGAGGAGTGA 439
DB 425 TCCAGGAGTGA 436

RESULT 11
US-10-447-315-20
; Sequence 20, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Heissig, Beate
; APPLICANT: Rafii, Shahin
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-447-315-20

Query Match 60.4%; Score 276.8; DB 17; Length 781;
Best Local Similarity 77.5%; Pred. No. 1.2e-62;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 8 GGATGACACACACACCACTCTCTCGGATCGAGGCGCGATGGCGCGCGCA 67
DB 37 GGCTGACAGGCTGTGCTCTTGGCACTGTGGCTGCGCATCTCTGACCCCGCGCT 96
QY 68 GCCGAGCCCGTCCACCCAGCGCTGGAGCGGTGAACGCGATCCAGGAGGCCCGCAGGC 127
DB 97 CGCCAGCCCCAGCAGCGCCCTGGAGCATGTGAATGCCATCCAGGAGGCCCGCGTC 156

QY 128 TCCTCAACCTCTCCCGGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
DB 157 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATCTCAG 216
QY 188 AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGCTGTACAAGCAGG 247
DB 217 AATGTTTGAACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAAGCAGG 276
QY 248 GCCTCCGCGGACCTCACCAGCTCAAGGCGCCGCTCACCATGATGGGCTCCCACTACA 307
DB 277 GCCTGCGGGGACGCTCACCAGCTCAAGGCGCCCTTGACCATGATGGCCAGCCACTACA 336
QY 308 AGCAGACTGCCCCACCGACCCCGGAGACCTCTGCGCCACCCAGATCATCACTTCGAGA 367
DB 337 AGCAGACTGCCCCACCGGAGAACTTCTGTGTCAACCCAGATTATCACTTTGAAA 396
QY 368 GCTTCAAGGAGACCTCAAGGACTTCTCTCTGATCCGTTTCGACTGCTGGAGCCGG 427
DB 397 GTTTCAAAGAGAACCTGAAGGACTTCTGCTGTGATCCCTTTGACTGCTGGAGCCAG 456
QY 428 TGCAGGAGTGAG 439
DB 457 TCCAGGAGTGAG 468

RESULT 12

US-10-131-985-16
; Sequence 16, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-985-16

Query Match 60.4%; Score 276.8; DB 16; Length 789;
Best Local Similarity 77.5%; Pred. No. 1.2e-62;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 8 GGATGCACCAACCAACCACTCTCTCGGATCGAGGCGCGCATGGCGCAGCGCGCA 67
DB 37 GGCTGCAGAGCTGTGCTCTTGGGCACTGTGGCTTGAGCATCTCTGCACCGCCCGCT 96
QY 68 GCCGAGCCCGTCCACCGAGCCGTCGGAGCAGCTGAACCGGATCCAGGAGGCCCGCAGGC 127
DB 97 CGCCAGCCCCAGCAGCGCCCTGGAGCATGTGAATGCCATCCAGGAGGCCCGCGTC 156
QY 128 TCCTCAACCTCTCCCGGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
DB 157 TCCTGAACCTGAGTAGAGACACTGCTGTGATGAATGAATGAACAGTAGAAGTCATCTCAG 216
QY 188 AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGCTGTACAAGCAGG 247
DB 217 AATGTTTGAACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAGCTGTACAAGCAGG 276
QY 248 GCCTCAACCTCTCCCGGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
DB 157 TCCTGAACCTGAGTAGAGACACTGCTGTGATGAATGAATGAACAGTAGAAGTCATCTCAG 216
QY 188 AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGCTGTACAAGCAGG 247
DB 217 AATGTTTGAACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAGCTGTACAAGCAGG 276

QY 248 GCCTCCGCGGACCTCACCAGCTCAAGGCGCCGCTCACCATGATGGGTCCCACTACA 307
DB 277 GCCTGCGGGGACGCTCACCAGCTCAAGGCGCCCTTGACCATGATGGCCAGCCACTACA 336
QY 308 AGCAGACTGCCCCACCGGAGACCTCTGCGCCACCCAGATCATCACTTCGAGA 367
DB 337 AGCAGACTGCCCCACCGGAGAACTTCTGTGTCAACCCAGATTATCACTTTGAAA 396
QY 368 GCTTCAAGGAGACCTCAAGGACTTCTCTCTGATCCGTTTCGACTGCTGGAGCCGG 427
DB 397 GTTTCAAAGAGAACCTGAAGGACTTCTGCTGTGATCCCTTTGACTGCTGGAGCCAG 456
QY 428 TGCAGGAGTGAG 439
DB 457 TCCAGGAGTGAG 468

RESULT 13

US-10-901-417-16
; Sequence 16, Application US/10901417
; Publication No. US20050026836A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; PRIOR FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-901-417-16

Query Match 60.4%; Score 276.8; DB 19; Length 789;
Best Local Similarity 77.5%; Pred. No. 1.2e-62;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 8 GGATGCACCAACCAACCACTCTCTCGGATCGAGGCGCGCATGGCGCAGCGCGCA 67
DB 37 GGCTGCAGAGCTGTGCTCTTGGGCACTGTGGCTTGAGCATCTCTGCACCGCCCGCT 96
QY 68 GCCGAGCCCGTCCACCGAGCCGTCGGAGCAGCTGAACCGGATCCAGGAGGCCCGCAGGC 127
DB 97 CGCCAGCCCCAGCAGCGCCCTGGAGCATGTGAATGCCATCCAGGAGGCCCGCGTC 156
QY 128 TCCTCAACCTCTCCCGGACACCGCCGCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
DB 157 TCCTGAACCTGAGTAGAGACACTGCTGTGATGAATGAATGAACAGTAGAAGTCATCTCAG 216
QY 188 AGATGTTGATCTCCAGGAGCCGACCTGCTCCAGACCCGCTCGAGCTGTACAAGCAGG 247
DB 217 AATGTTTGAACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAGCTGTACAAGCAGG 276
QY 248 GCCTCCGCGGACCTCACCAGCTCAAGGCGCCGCTCACCATGATGGGCTGCCACTACA 307
DB 277 GCCTGCGGGGACGCTCACCAGCTCAAGGCGCCCTTGACCATGATGGCCAGCCACTACA 336
QY 308 AGCAGACTGCCCCACCGGAGACCTCTGCGCCACCCAGATCATCACTTCGAGA 367
DB 337 AGCAGACTGCCCCCAACCCCGGAACTTCTGTGTGAACCCAGATTATCACTTTGAAA 396

Search completed: March 11, 2005, 18:28:48
Job time : 457 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 17:24:26 ; Search time 473 Seconds

(without alignments)
1777.174 Million cell updates/sec

Title: US-10-723-083-2

Perfect score: 765

Sequence: 1 MHHHHSSGIEGRMAPARS.....ENLKDFLLVPPDCWEPVQE 142

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cpn2.1/USPTO.spool/US10723083/runat_08032005_131715_10414/app.query.fasta_1.327
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10723083 @CGN 1.1 644 @runat_08032005_131715_10414 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
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3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	89.2	777	2	Aaq97169 pMON13022
2	682	89.2	777	3	Aaa03723 Human int
3	682	89.2	777	6	Abx00012 Human int
4	682	89.2	777	12	Adj14267 DNA relat
5	679	88.8	1610	2	Aat72724 p53-GM-CS

6	678	88.6	384	2	AAT34400	Aat34400 Granulocy
7	678	88.6	384	2	ABA96672	Aba96672 Human gra
8	678	88.6	402	2	AAQ97208	Aaq97208 pMON13012
9	678	88.6	402	3	AAA03771	Aaa03771 Human G-C
10	678	88.6	402	6	ABX00086	Abx00086 Human int
11	678	88.6	402	12	ADJ14388	Adj14388 DNA relat
12	678	88.6	410	1	AAH81322	Aah81322 Synthetic
13	678	88.6	415	1	AAH90383	Aah90383 Synthetic
14	678	88.6	415	1	AAH90274	Aah90274 Synthetic
15	678	88.6	822	2	AAQ97183	Aaq97183 pMON13035
16	678	88.6	822	3	AAA03737	Aaa03737 Human int
17	678	88.6	822	6	ABX00026	Abx00026 Human int
18	678	88.6	822	12	ADJ14281	Adj14281 DNA relat
19	678	88.6	903	2	AAQ97180	Aaq97180 pMON13031
20	678	88.6	903	3	AAA03734	Aaa03734 Human int
21	678	88.6	903	6	ABX00023	Abx00023 Human int
22	678	88.6	903	12	ADJ14278	Adj14278 DNA relat
23	676	88.4	1630	3	AAZ50587	Aaz50587 HD70scFv-
24	675	88.2	2211	12	ADL16719	Adl16719 Human stu
25	673	88.0	381	3	AAZ88268	Aaz88268 Granulocy
26	673	88.0	384	2	AAT34399	Aat34399 Granulocy
27	673	88.0	410	1	AAH81320	Aah81320 Sequence
28	673	88.0	429	12	ADJ36194	Adj36194 Self-coal
29	673	88.0	435	2	AAV83189	Aav83189 Granulocy
30	673	88.0	435	3	AAA64392	Aaa64392 DNA seque
31	673	88.0	435	10	ADF15808	Adf15808 Human alb
32	673	88.0	435	10	ADF15714	Adf15714 Human alb
33	673	88.0	435	10	ADF15807	Adf15807 Human alb
34	673	88.0	435	10	ADF15715	Adf15715 Human alb
35	673	88.0	435	10	ACC78877	Acc78877 Human GM-
36	673	88.0	435	12	ADI20788	Adi20788 Human GM-
37	673	88.0	435	12	ADI20789	Adi20789 Human GM-
38	673	88.0	435	12	ADN49689	Adn49689 Human gra
39	673	88.0	435	12	ADQ76022	Adq76022 Human GM-
40	673	88.0	435	12	ADQ76023	Adq76023 Human GM-
41	673	88.0	440	1	AAH81321	Aah81321 Sequence
42	673	88.0	448	12	ADL16729	Adl16729 Human gra
43	673	88.0	505	13	ADS88046	Ads88046 Tumour tr
44	673	88.0	579	12	ADJ36238	Adj36238 Self-coal
45	673	88.0	661	1	AAH70561	Aah70561 Sequence

ALIGNMENTS

RESULT 1
AAQ97169
ID AAQ97169 standard; DNA; 777 BP.
XX
AC AAQ97169;
XX
DT 25-AUG-1999 (first entry)
XX
DE pMON13022 DNA encoding IL-3 fusion protein.
XX
KW Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9521254-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US001185.
XX
PR 04-FEB-1994; 94US-00192325.
XX
(SEAR) SEARLE & CO G D.
XX
PA Aaq97169 pMON13022
XX
PI Aaa03723 Human int
XX
PI Abx00012 Human int
XX
PI Adj14267 DNA relat
XX
PI Aat72724 p53-GM-CS

DR WPI: 1995-283774/37.
 XX P-PSDB; AAR79317.
 XX Fusion proteins comprising a human interleukin-3 variant, a linker and
 PT interleukin-3, a variant of a colony stimulating factor - useful to
 PT increase haematopoietic cell prodn. in a mammal.
 XX
 PS Claim 22; Page 158-159; 447pp; English.
 XX
 CC A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
 CC R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
 CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
 CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
 CC or IL-3 variant, and L is a linker. Generic sequences are described in
 CC AA03235 - AA03242, and specifically claimed examples are shown in
 CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
 CC recombinant DNA techniques. Specifically claimed examples of DNA
 CC sequences (including the present sequence) which encode these proteins
 CC are shown in AA097167-Q97204 and AA097222-Q97227. The fusion protein is
 CC used to increase haematopoietic cell production. It is also useful as an
 CC IL-3 antagonist or as a discrete antigenic fragment for production of
 CC antibodies useful in immunoassays and immunotherapy. Antagonists are used
 CC to block the growth of certain cancer cells and in treatment of asthma.
 CC The fusion protein can also be used to stimulate bone marrow and blood
 CC cell activation and growth in vitro before infusion; and to treat
 CC diseases characterised by decreased levels of myeloid, erythroid,
 CC lymphoid and/or megakaryocyte cells of the haematopoietic system. The
 CC protein has the usual activity of both its component proteins, but may
 CC have increased synergistic activity and reduced undesired side effects
 XX
 SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.38e-67 Length: 777
 Score: 682.00 Matches: 130
 Percent Similarity: 97.01% Conservative: 0
 Best Local Similarity: 97.01% Mismatches: 4
 Query Match: 89.15% Indels: 0
 DB: 2 Gaps: 0

US-10-723-083-2 (1-142) x AAQ97169 (1-777)

QY 9 SerGlylleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
 Db 376 TCTGGGGGGGGCTCCCAACATGGACCGGCTCGTTCCTCCCGCTCCCGCTACCCAGCGGTGG 435
 QY 29 GluHisValAsnAlaIleGlnGluAlaArgAtcLeuLeuAsnLeuSerArgAspThrAla 48
 Db 436 GAACACGTGATGATCCATCCAGGAGGCGCGCGTCTCTGAACCTGAGTAGAGACACTGTCT 495
 QY 49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
 Db 496 GCTGAGATGAATGAACACAGTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGCAT 555
 QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
 Db 556 TGCCTACAGACCGCGCTGGAGCTGTACAAGCAGGCGCTCGGGGCGAGCCTCACCAGCTC 615
 QY 89 LysGlyProLeuThrMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
 Db 616 AAGGGCCCTTGAATGATGGCCAGCCACTACAAGCAGACTGCGCTCAACCCCGGAA 675
 QY 109 ThrSerCysAlaThrGlnIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
 Db 676 ACTTCTGTGCAACCCAGATATACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTC 735
 QY 129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
 Db 736 CTGCTGTTCATCCCTTTGACTCTCGGAGCCAGTCCAGGAG 777

RESULT 2

AAA03723

ID AAA03723 standard; DNA; 777 BP.

XX AAA03723;
 AC 19-MAY-2000 (first entry)
 DT Human interleukin-3 mutant containing fusion protein DNA SEQ ID NO:55.
 DE
 XX Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;
 KW radiation therapy; chemotherapy; bone marrow suppressive drug;
 KW bone marrow activation; blood cell activation; blood transplant; ds.
 XX Homo sapiens.
 OS Synthetic.
 XX US6022535-A.
 PN 08-FEB-2000.
 XX 06-JUN-1995; 95US-00469318.
 PF 04-FEB-1994; 94US-00192325.
 PR 02-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95US-00411795.
 XX (SEAR) SEARLE & CO G D.
 PA
 XX Bauer SC, Abrams MA, Brafard-Goldberg SR, Easton AM, Klein BK;
 PI Paik K, Thomas JW, McKearn JP, Olins PO, Caparon MH;
 PI WPI; 2000-160368/14.
 DR
 XX Treating hematopoietic disorders with fusion proteins comprising mutated
 PT interleukin-3 fused with secondary colony stimulating factors or other
 PT interleukin-3 variants.
 XX
 PS Example 27; Col 135-136; 276pp; English.
 XX
 CC Methods have been developed for treating haematopoietic disorders with
 CC fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
 CC 3) variants or mutant proteins (muteins) fused with secondary colony
 CC stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
 CC and/or haematopoietic colony stimulating factors) or other interleukin-3
 CC variants with or without a linker. The methods may be used in vivo to
 CC treat haematopoietic disorders resulting from bacterial, viral and fungal
 CC infections, cancer radiation therapy, chemotherapy or bone marrow
 CC suppressive drugs. They may also be used in vitro to stimulate bone
 CC marrow and blood cell activation and growth prior to infusion of the bone
 CC marrow and blood transplants into patients. IL-3 is a haematopoietic
 CC growth factor which has the property of being able to promote the
 CC survival, growth and differentiation of haematopoietic cells. The fusion
 CC molecules are characterised by possessing the usual activity of both of
 CC their constituent peptides and further by having a biological or
 CC physiological activity greater than the additive function of the IL-3 or
 CC second CSF alone (i.e. the peptides act synergistically). Their activity
 CC may also be further enhanced by the mutations they comprise. The
 CC variations may further reduce undesirable side effects associated with IL
 CC -3. AA053130 to AA053226, and AA03721 to AA03782 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.38e-67 Length: 777
 Score: 682.00 Matches: 130
 Percent Similarity: 97.01% Conservative: 0
 Best Local Similarity: 97.01% Mismatches: 4
 Query Match: 89.15% Indels: 0
 DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x AAA03723 (1-777)

QY 9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTyr 28
 DB 376 TCTGGCGCGCGCTCCAACTGGCAGCGCTCGTTCCCGCTCCCGCTACCCAGCGGTGG 435
 QY 29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
 DB 436 GAACACGTGAATGCCATCCAGGAGGCCCGCGCTCTCTGAACCTGAGTAGAGACACTGCT 495
 QY 49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
 DB 496 GCTGAGATGAATGAACAGTAGAAGTATCATCAAAATGTTTTCACCTCCAGGAGCGCACT 555
 QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
 DB 556 TGCCTACAGACCGCGCTGGAGCTGTACAAGCAGGCGCTCGGGGCGAGCTCCACCAAGCTC 615
 QY 89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProThrProGlu 108
 DB 616 AAGGGCCCTTGACATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAAACCCCGGAA 675
 QY 109 ThrSerCysAlaThrGlnIleThrPheGluSerPheLysGluLeuLysAspPhe 128
 DB 676 ACTTCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAGAGAACTCGAAGGACTTC 735
 QY 129 LeuLeuValIleProPheAspCysTyrGluProValGlnGlu 142
 DB 736 CTGCTTGTATCCCTTTGACTGCTGGAGCCAGTCCAGGAG 777

RESULT 3 ABX00012

ID ABX00012 standard; DNA; 777 BP.

XX AC ABX00012;
 XX 18-DEC-2002 (first entry)
 XX Human interleukin-3 associated DNA sequence #3.
 XX
 KW Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds;
 KW G-CSF; G-CSFser17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
 KW human growth hormone; B-cell growth factor; leukaemia;
 KW B-cell differentiation factor; eosinophil differentiation factor;
 KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
 KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
 KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
 KW myelofibrosis; Interleukin-3; IL-3; stem cell.
 XX
 OS Unidentified.
 XX
 PN US6436387-B1.
 XX
 PD 20-AUG-2002.
 XX
 PF 09-DEC-1996; 96US-00762227.
 XX
 PR 24-NOV-1992; 92US-00981044.
 PR 22-NOV-1993; 93WO-US011197.
 PR 04-FEB-1994; 94US-00192325.
 PR 04-FEB-1995; 95WO-US0001185.
 PR 06-APR-1995; 95US-00411795.
 PR 06-JUN-1995; 95US-00446872.
 XX
 PA (SEAR) SEARLE & CO G D.

XX
 PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;
 XX
 DR WPI; 2002-749206/81.

XX Ex vivo expansion of stem cells, for enhancing transduction efficiency of
 PT cultured stem cells, comprises culturing stem cells in growth-medium
 PT having mutant interleukin-3, and hematopoietic factor, and harvesting
 PT cultured cells.

XX Disclosure; Col 161-164; 203pp; English.

XX The invention relates to ex vivo expansion of stem cells, comprises
 CC culturing stem cells with a growth medium comprising a chimera protein,
 CC and harvesting the cultured stem cells. The chimera is based on a
 CC mutated human interleukin-3 (IL-3) sequence coupled to a haematopoietic
 CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
 CC CSFser17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
 CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
 CC differentiation factor, eosinophil differentiation factor and stem cell
 CC factor (SCF)) via a peptide linker. The formula for the chimera is given
 CC in the specification. Also included is a method for enhancing the
 CC efficiency of the transduction of cultured stem cells by a heterologous
 CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
 CC culturing the stem cells with a growth medium comprising the chimera (c)
 CC transducing DNA into cultured cells; and (d) harvesting the transduced
 CC cells. The method is useful for ex vivo expansion of stem cells, and
 CC enhancing the efficiency of the transduction of cultured stem cells by a
 CC heterologous gene. The method is also useful for treating a patient
 CC having a haematopoietic disorder. The expanded haematopoietic cells are
 CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
 CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
 CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
 CC and myelofibrosis. The present sequence is an IL-3 mutant associated DNA
 CC sequence. Note: The present sequence is included in the sequence listing
 CC but is not mentioned anywhere else in the specification
 XX

SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.38e-67 Length: 777
 Score: 682.00 Matches: 130
 Percent Similarity: 97.01% Conservative: 0
 Best Local Similarity: 97.01% Mismatches: 4
 Query Match: 89.15% Indels: 0
 DB: 6 Gaps: 0

US-10-723-083-2 (1-142) x ABX00012 (1-777)

QY 9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTyr 28
 DB 376 TCTGGCGCGCGCTCCAACTGGCAGCGCTCGTTCCCGCTCCCGCTACCCAGCGGTGG 435
 QY 29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
 DB 436 GAACACGTGAATGCCATCCAGGAGGCCCGCGCTCTCTGAACCTGAGTAGAGACACTGCT 495
 QY 49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
 DB 496 GCTGAGATGAATGAACAGTAGAAGTATCATCAAAATGTTTTCACCTCCAGGAGCGCACT 555
 QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
 DB 556 TGCCTACAGACCGCGCTGGAGCTGTACAAGCAGGCGCTCGGGGCGAGCTCCACCAAGCTC 615
 QY 89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProThrProGlu 108
 DB 616 AAGGGCCCTTGACATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAAACCCCGGAA 675
 QY 109 ThrSerCysAlaThrGlnIleThrPheGluSerPheLysGluLeuLysAspPhe 128
 DB 676 ACTTCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAGAGAACTCGAAGGACTTC 735
 QY 129 LeuLeuValIleProPheAspCysTyrGluProValGlnGlu 142
 DB 736 CTGCTTGTATCCCTTTGACTGCTGGAGCCAGTCCAGGAG 777

RESULT 4

ID ADJ14267
 XX ADJ14267 standard; DNA; 777 BP.
 AC ADJ14267;

XX DT 20-MAY-2004 (first entry)
XX DE DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 55.
XX KW stem cell; antianemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.
XX OS Unidentified.
XX PN US2003185790-A1.
XX PD 02-OCT-2003.
XX PF 26-FEB-2002; 2002US-00083446.
XX PR 24-NOV-1992; 92US-00981044.
XX PR 22-NOV-1993; 93WO-US011197.
XX PR 04-FEB-1994; 94US-00192325.
XX PR 02-FEB-1995; 95WO-US001185.
XX PR 06-APR-1995; 95US-00411795.
XX PR 06-JUN-1995; 95US-00446872.
XX PR 09-DEC-1996; 96US-00762227.
XX PA (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAF/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX WPI; 2004-096775/10.
XX EX vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT aplastic anemia, involves culturing the stem cells with growth medium
PT comprising chimera protein, and harvesting the cultured stem cells.
XX PS Disclosure; SEQ ID NO 55; 202pp; English.
XX CC The invention relates to a novel method whereby stem cells are ex vivo
CC expanded via culturing the stem cells with a growth medium comprising a
CC chimera protein, followed by harvesting of the cultured stem cells. The
CC method of the invention has antianemic, immunostimulant,
CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC cytostatic and neuroprotective applications and may be useful to target
CC haemopoietic cells for gene therapy, preferably for treating patients
CC having a haemopoietic disorder characterised by decreased levels of
CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC system. The expanded ex vivo cells may be used to treat neutropenia,
CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC myelofibrosis. The current sequence is that of a DNA related to the human
CC interleukin-3 (IL-3) mutant protein of the invention.
XX SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.38e-67 Length: 777
Score: 682.00 Matches: 130
Percent Similarity: 97.01% Conservative: 0
Best Local Similarity: 97.01% Mismatches: 4
Query Match: 89.15% Indels: 0

DB: 12 Gaps: 0
US-10-723-083-2 (1-142) x ADJ14267 (1-777)
QY 9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
DB 376 TCTGGCGGGCTCAACATGCGACGGCTCGTTCCCGCTCCCGTCTACCCAGCGGTGG 435
QY 29 GluHisValAspAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
DB 436 GAACAGTGAATGCCATCCAGGAGGCCCGCGCTCTCTGAACCTGAGTAGACACTGCT 495
QY 49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnProThr 68
DB 496 GCTGAGATGAATGAAACAGTAGAAGTATATCAGAAATGTTTGACCTCCAGGAGCGGACT 555
QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
DB 556 TGCCTACAGACCGCGCTGGAGCTGTACAGACGAGGCGCTCGGGGCGACGCTCACAAGCTC 615
QY 89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
DB 616 AAGGGCCCTTGACCATGATGCGCCACTACAAGCAGACTGCCCTCCAACCCCGGAA 675
QY 109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
DB 676 ACTTCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTC 735
QY 129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
DB 736 CTGCTTGTCATCCCTTTGACTGTGGGAGCAGCTCCAGGAG 777
RESULT 5
AAT72724
ID AAT72724 standard; cDNA; 1610 BP.
XX AC AAT72724;
XX DT 17-SEP-1997 (first entry)
XX DE p53-GM-CSF immunostimulant fusion protein DNA.
KW p53-GM-CSF; granulocyte macrophage colony stimulating factor;
KW tumour suppressor gene; immunostimulant; cancer; therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 9..1610
FT /tag= a
FT /product= "p53-GM-CSF fusion protein"
FT mRNA 9..1187
FT /tag= b
FT /product= "p53"
FT mRNA 1188..1193
FT /tag= c
FT /product= "Ser-Arg linker"
FT mRNA 1194..1610
FT /tag= d
FT /product= "GM-CSF"
XX WO9724438-A1.
XX PN 10-JUL-1997.
XX PD 23-DEC-1996; 96WO-US020241.
XX PR 28-DEC-1995; 95US-00579823.
XX PA (ACTI-) ACTIVATED CELL THERAPY INC.
XX PI Laus R, Ruegg CL, Wu H;
XX

DR WPI; 1997-363674/33.
 XX P-PSDB; AAW19763.
 PT Potent APC that activates T-cells to give multivalent cellular immune
 PT response - can also induce a cytotoxic T-cell response in a vertebrate
 XX subject.
 XX
 PS Example 7; Fig 11; 45pp; English.
 XX
 CC A nucleic acid molecule (AA72724) codes for a fusion protein (AAW19763)
 CC comprising human p53 tumour suppressor protein and granulocyte-macrophage
 CC colony stimulating factor (GM-CSF). It was prep'd. by PCR amplification of
 CC p53 cDNA GM-CSF cDNA sequences (the GM-CSF antisense primer including a
 CC hexahistidine tag sequence) and their fusion via a XbaI linker. Fusion
 CC expression vectors can be used to transfect mammalian and insect cells.
 CC The p53-GM-CSF fusion protein is used to generate anti-p53 immunity.
 CC Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo
 CC or in vitro by exposure to antigen-presenting cells exposed to the fusion
 CC protein
 XX
 SQ Sequence 1610 BP; 383 A; 508 C; 407 G; 312 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8-21e-67 Length: 1610
 Score: 679.00 Matches: 128
 Percent Similarity: 98.47% Conservative: 1
 Best Local Similarity: 97.71% Mismatches: 2
 Query Match: 88.76% Indels: 0
 DB: 2 Gaps: 0
 US-10-723-083-2 (1-142) x AAT72724 (1-1610)
 QY 12 GluGlyArgMetAlaProAlaArgSerProSerThrGlnProTrpGluHisVal 31
 DB 1185 GACTCTAGATCGCACCCGCCGCTCGCCAGCCAGCACAGCCCTGGGAGCATGTG 1244
 QY 32 AsnAlaIleGlnLalaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMet 51
 DB 1245 AATGCCATCCAGAGGCCCGCGCTCTCTGAACCTGAGTAGACACTGCTGTGAGATG 1304
 QY 52 AsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGln 71
 DB 1305 NATGAACAGTAGAGTATCTCAGAAATGTTTGACTCTCAGAGCGGACCTGCTACAG 1364
 QY 72 ThrArgLeuGluLeuTrpLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyPro 91
 DB 1365 ACCCGCTCGAGCTGTACAAGCAGGCGCTCGCGGCGAGCCTCACCAAGCTCAAGGCGCCC 1424
 QY 92 LeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCys 111
 DB 1425 TTGACCATGATGCCAGCCCACTACAACAGCAGCTGCCCTCCAAACCCCGGAAACTTCTGT 1484
 QY 112 AlaThrGlnIleIleThrPheGluSerPheLeuGluAsnLeuLysAspPheLeuVal 131
 DB 1485 GCNAACCCAGATTATCACTTTGAAAGTTTCAAGAGAACTGAAGGACTTCTGCTGTTC 1544
 QY 132 IleProPheAspCysTrpGluProValGlnGlu 142
 DB 1545 ATCCCTTTGACTGCTGGGAGCCAGCCAGGAG 1577
 RESULT 6
 AAT34400
 ID AAT34400 standard; DNA; 384 BP.
 XX
 AC AAT34400;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 11-FEB-1997 (first entry)
 XX
 DE Granulocyte macrophage colony-stimulating factor coding sequence.
 XX
 XX GM-CSF; granulocyte macrophage colony-stimulating factor; expression;
 KW construct; stable; production; ds.

XX Homo sapiens.
 XX JP08173185-A.
 PN
 PD 09-JUL-1996.
 XX
 PF 28-APR-1987; 95JP-00263370.
 XX
 PR 28-APR-1987; 87JP-00106148.
 XX
 PA (AMGE-) AMGEN INC.
 PA (KIRI) KIRIN BREWERY KK.
 XX
 DR WPI; 1996-365600/37..
 DR N-PSDB; AAW00103.
 XX
 PT Prodn. of human granulocyte macrophage colony-stimulating factor - by
 PT culturing E. coli transformed with human GM-CSF DNA.
 XX
 PS Claim 1; Page 2; 16pp; Japanese.
 XX
 CC The present sequence encodes human granulocyte macrophage colony-
 CC stimulating factor (hGM-CSF; n = 101, Ile). A series of oligonucleotides
 CC were synthesised and ligated together to form a stable expression
 CC construct. The technique is used for the efficient prodn. of a
 CC glycoprotein with hGM-CSF activity. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 384 BP; 101 A; 100 C; 86 G; 97 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.5e-67 Length: 384
 Score: 678.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.63% Indels: 0
 DB: 2 Gaps: 0
 US-10-723-083-2 (1-142) x AAT34400 (1-384)
 QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
 DB 1 ATGGCACCCAGCTCGATCACCGTCCGCTCCACTCAACCATGGGAACATGTTAACGCAATC 60
 QY 35 GlnGluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
 DB 61 CAGGAAGCTCGTCTGCTGTGTAACCTGCTCGTACTGCTGCTGAAATGAACGAACT 120
 QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
 DB 121 GTTGAAGTGATCAGCGAAATGTTGATCTGCAGGAACCGACTTGTCTGCAACCCGCTCTG 180
 QY 75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
 DB 181 GAACTGTACAAACAAGGCTGCGTGGTCTCTGACTAAACTGAAGGTCGCTGACTATG 240
 QY 95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
 DB 241 ATGGCTAGCCATTACAAACAGCATTTGTCGCCGACTCCGGAAACTTCTTGTGTACTCTAG 300
 QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
 DB 301 ATCATCACTTTCGAATCTTTCAAGAGAAACCTGAAAGATTCTCTGCTGGTTATCCCGTTC 360
 QY 135 AspCysTrpGluProValGlnGlu 142
 DB 361 GATTGTGGAAACCGGTTTCAGGAA 384
 RESULT 7
 ABA96672
 ID ABA96672 standard; cDNA; 384 BP.
 XX

AC ABA96672;
 XX 23-APR-2002 (first entry)
 XX Human granulocyte macrophage-colony stimulating factor (hGM-CSF) cDNA.
 XX Human; GM-CSF; granulocyte macrophage-colony stimulating factor;
 KW recombinant production; Escherichia coli; pET-11d vector; gene; ds.
 XX Homo sapiens.
 XX KR98053420-A.
 XX 25-SEP-1998.
 XX 26-DEC-1996; 96KR-00072523.
 XX 26-DEC-1996; 96KR-00072523.
 XX (CHEI-) CHEIL FOODS & CHEM INC.
 XX Ahn DH, Lee HS, Mok H, Hah SH, Koh HG, Oh MS, Kim HS;
 XX WPI; 1999-517067/43.
 XX Human granulocyte macrophage-colony stimulating factor.
 XX Example 1; Fig 4; 7pp; Korean.
 XX The invention relates to the recombinant production of human granulocyte
 CC macrophage-colony stimulating factor (hGM-CSF). NcoI and BamHI
 CC restriction sites were inserted into hGM-CSF cDNA (ABA96672) via PCR
 CC using primers ABA96670-ABA96671, prior to cleavage with these enzymes and
 CC insertion into the pET-11d vector downstream of the T7/lac promoter to
 CC form the plasmid pT7GMCSP. pT7GMCSP was transformed into Escherichia coli
 CC BL21 (DE3) plys for recombinant expression of hGM-CSF. The present
 CC sequence represents hGM-CSF cDNA
 XX
 SQ Sequence 384 BP; 93 A; 125 C; 97 G; 69 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.5e-67 Length: 384
 Score: 678.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.63% Indels: 0
 DB: 2 Gaps: 0
 US-10-723-083-2 (1-142) x ABA96672 (1-384)
 QY 15 MetAlaProAlaArgSerProSerThrGlnProThrGluHisValAsnAlaIle 34
 Db 1 ATGGCACCCGCGCTCGCCAGCCGCCAGCAGCCCTGGAGCATGTGATGCCATC 60
 QY 35 GlnGluAlaArgGluLeuLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
 Db 61 CAGGAGCCCGCGCTCTCTGAACCTGAGTAGAGACACTGCTGAGATGAATAA 120
 QY 55 ValGluValIleSerGluMetPheAspLeuGlnProThrCysLeuGlnThrArgLeu 74
 Db 121 GTAGAGATCATCTCAGAAATGTTGACCTCCAGGAGCCGACTGCTCAGACCCGCTG 180
 QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
 Db 181 GAGCTGTACAGCAGGCGCTCGGGGCGAGCCTCACCAGCTCAAGGGCCCTTGACCATG 240
 QY 95 MetAlaSerHisTyrlsGlnHisCysProThrProGluThrSerCysAlaThrGln 114
 Db 241 ATGGCCAGCACTTACAGAGCAGCACTGCCCTCCAAACCCGGAACCTTCTGTGCAACCCAG 300
 QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
 Db 301 ATATACACCTTTGAAAGTTTCAAGAGAACCTTGAGGACTTTTCTGCTTGTATCCCTTT 360

QY 135 AspCysTrpGluProValGlnGlu 142
 Db 361 GACTGCTGGAGCCAGTCCAGGAG 384
 RESULT 8
 AAQ97208
 ID AAQ97208 standard; DNA; 402 BP.
 XX AAQ97208;
 XX 25-AUG-1999 (first entry)
 XX pMON13012 DNA sequence.
 XX Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
 KW mutant; mutein; fusion protein; linker; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9521254-A1.
 XX 10-AUG-1995.
 XX 02-FEB-1995; 95WO-US001185.
 XX 04-FEB-1994; 94US-00192325.
 XX (SEAR) SEARLE & CO G D.
 XX Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 PI Klein BK, McKearn JP, Ollins PO, Paik K, Thomas JW;
 XX WPI; 1995-283774/37.
 XX P-PSDB; AAR79338.
 XX Fusion proteins comprising a human interleukin-3 variant, a linker and
 PT interleukin-3, a variant or a colony stimulating factor - useful to
 PT increase haematopoietic cell prodn. in a mammal.
 XX Example 19; Page 183; 447pp; English.
 XX A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
 CC R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
 CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
 CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
 CC or IL-3 variant, and L is a linker. Generic sequences are described in
 CC AA03235 - AA003242, and specifically claimed examples are shown in
 CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
 CC recombinant DNA techniques. Specifically claimed examples of DNA
 CC sequences which encode these proteins are shown in AAQ97167-Q97204 and
 CC AAQ97222-Q97227. The fusion protein is used to increase haematopoietic
 CC cell production. It is also useful as an IL-3 antagonist or as a discrete
 CC antigenic fragment for production of antibodies useful in immunoassays
 CC and immunotherapy. Antagonists are used to block the growth of certain
 CC cancer cells and in treatment of asthma. The fusion protein can also be
 CC used to stimulate bone marrow and blood cell activation and growth in
 CC vitro before infusion; and to treat diseases characterised by decreased
 CC levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the
 CC haematopoietic system. The protein has the usual activity of both its
 CC component proteins, but may have increased synergistic activity and
 CC reduced undesired side effects
 XX
 SQ Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.59e-67 Length: 402
 Score: 678.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.63% Indels: 0
 DB: 2 Gaps: 0

US-10-723-083-2 (1-142) x AAQ97208 (1-402)

QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
 Db 1 ATGGCACCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACAGTGAATGCCATC 60

QY 35 GlnGluAlaArgGlnLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
 Db 61 CAGGAGCGCGGGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAACA 120

QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
 Db 121 GTAGAAGTATATCAGAAATGTTTGAACCTGAGTGGGCGGCTGCTGCTGAGATGAACA 180

QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
 Db 181 GAGCTGTACAGCGGCGCTGCGGGCAGCTTACCAAGCTCAAGGGCCCCCTTGACCATG 240

QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
 Db 241 ATGGCCAGCCACTACAAAGCAGCAGCTGCCCTCCAAACCCCGGAACTTCTGTGCAACCCAG 300

QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
 Db 301 ATTATCACCTTTGAAAGTTCAAAGAGAACCTGAGGACTTCTGCTTGTGTCATCCCTTT 360

QY 135 AspCysTrpGluProValGlnGlu 142
 Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 9
 AAA03771
 ID AAA03771 standard; DNA; 402 BP.
 AC AAA03771;
 DT 19-MAY-2000 (first entry)
 DE Human G-CSF mutant DNA sequence SEQ ID NO:176.
 KW Human; interleukin 3; IL-3; mutant; mutin; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;
 KW radiation therapy; chemotherapy; bone marrow suppressive drug;
 KW bone marrow activation; blood cell activation; blood transplant; ds.
 OS Homo sapiens.
 OS Synthetic.
 XX US6022535-A.
 PN 08-FEB-2000.
 XX 06-JUN-1995; 95US-00469318.
 XX 04-FEB-1994; 94US-00192325.
 PR 02-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95US-00411795.
 XX (SEAR) SEARLE & CO G D.
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
 PI Paik K, Thomas JW, McKearn JP, Olines PO, Caparon MH;
 XX WPI; 2000-160368/14.
 DR Treating hematopoietic disorders with fusion proteins comprising mutated
 PT interleukin-3 fused with secondary colony stimulating factors or other
 PT interleukin-3 variants.
 XX Example 19; Col 171-174; 276pp; English.

Methods have been developed for treating haematopoietic disorders with fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-3) variants or mutant proteins (mutins) fused with secondary colony stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin-3 and/or haematopoietic colony stimulating factors) or other interleukin-3 variants with or without a linker. The methods may be used in vivo to treat haematopoietic disorders resulting from bacterial, viral and fungal infections, cancer radiation therapy, chemotherapy or bone marrow suppressive drugs. They may also be used in vitro to stimulate bone marrow and blood cell activation and growth prior to infusion of the bone marrow and blood transplants into patients. IL-3 is a haematopoietic growth factor which has the property of being able to promote the survival, growth and differentiation of haematopoietic cells. The fusion molecules are characterised by possessing the usual activity of both of their constituent peptides and further by having a biological or physiological activity greater than the additive function of the IL-3 or second CSF alone (i.e. the peptides act synergistically). Their activity may also be further enhanced by the mutations they comprise. The variations may further reduce undesirable side effects associated with IL-3. AA03771 to AA03782 represent sequences used in the exemplification of the present invention

Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.59e-67 Length: 402
 Score: 678.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.63% Indels: 0
 DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x AAA03771 (1-402)

QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
 Db 1 ATGGCACCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACAGTGAATGCCATC 60

QY 35 GlnGluAlaArgGlnLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
 Db 61 CAGGAGCGCGGGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAACA 120

QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
 Db 121 GTAGAAGTATATCAGAAATGTTTGAACCTGAGTGGGCGGCTGCTGCTGAGATGAACA 180

QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
 Db 181 GAGCTGTACAGCGGCGCTGCGGGCAGCTTACCAAGCTCAAGGGCCCCCTTGACCATG 240

QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
 Db 241 ATGGCCAGCCACTACAAAGCAGCAGCTGCCCTCCAAACCCCGGAACTTCTGTGCAACCCAG 300

QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
 Db 301 ATTATCACCTTTGAAAGTTCAAAGAGAACCTGAGGACTTCTGCTTGTGTCATCCCTTT 360

QY 135 AspCysTrpGluProValGlnGlu 142
 Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 9
 AAA03771
 ID AAA03771 standard; DNA; 402 BP.
 AC AAA03771;
 DT 19-MAY-2000 (first entry)
 DE Human G-CSF mutant DNA sequence SEQ ID NO:176.
 KW Human; interleukin 3; IL-3; mutant; mutin; CSF; cytokine;
 KW colony stimulating factor; haematopoietic growth factor; lymphokine;
 KW fusion protein; haematopoietic disorder; infection; cancer;
 KW radiation therapy; chemotherapy; bone marrow suppressive drug;
 KW bone marrow activation; blood cell activation; blood transplant; ds.
 OS Homo sapiens.
 OS Synthetic.
 XX US6022535-A.
 PN 08-FEB-2000.
 XX 06-JUN-1995; 95US-00469318.
 XX 04-FEB-1994; 94US-00192325.
 PR 02-FEB-1995; 95WO-US001185.
 PR 06-APR-1995; 95US-00411795.
 XX (SEAR) SEARLE & CO G D.
 XX Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
 PI Paik K, Thomas JW, McKearn JP, Olines PO, Caparon MH;
 XX WPI; 2000-160368/14.
 DR Treating hematopoietic disorders with fusion proteins comprising mutated
 PT interleukin-3 fused with secondary colony stimulating factors or other
 PT interleukin-3 variants.
 XX Example 19; Col 171-174; 276pp; English.

G-CSF; G-CSFser17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand; human growth hormone; B-cell growth factor; leukaemia; B-cell differentiation factor; eosinophil differentiation factor; stem cell factor; SCF; cyclic neutropenia; aplastic anaemia; thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome; systemic lupus erythematosus; SLE; myelodysplastic syndrome; myelofibrosis; Interleukin-3; IL-3; stem cell.

Unidentified.

US6436387-B1.

20-AUG-2002.

09-DEC-1996; 96US-00762227.

24-NOV-1992; 92US-00981044.

22-NOV-1993; 93WO-US011197.

04-FEB-1994; 94US-00192325.

04-FEB-1995; 95WO-US001185.

06-APR-1995; 95US-00411795.

06-JUN-1995; 95US-00446872.

(SEAR) SEARLE & CO G D.

Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM; Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;

WPI; 2002-749206/81.

Ex vivo expansion of stem cells, for enhancing transduction efficiency of cultured stem cells, comprises culturing stem cells in growth medium having mutant interleukin-3, and hematopoietic factor, and harvesting cultured cells.

Disclosure; Col 299-300; 203pp; English.

The invention relates to ex vivo expansion of stem cells, comprises culturing stem cells with a growth medium comprising a chimera protein, and harvesting the cultured stem cells. The chimera is based on a mutated human interleukin-3 (IL-3) sequence coupled to a haematopoietic factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-CSFser17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16, flt3 ligand, human growth hormone, B-cell growth factor, B-cell differentiation factor, eosinophil differentiation factor and stem cell factor (SCF)) via a peptide linker. The formula for the chimera is given in the specification. Also included is a method for enhancing the efficiency of the transduction of cultured stem cells by a heterologous gene, comprising: (a) removing stem cells from a patient or donor; (b) culturing the stem cells with a growth medium comprising the chimera (c) transducing DNA into cultured cells; and (d) harvesting the transduced cells. The method is useful for ex vivo expansion of stem cells, and enhancing the efficiency of the transduction of cultured stem cells by a heterologous gene. The method is also useful for treating a patient having a haematopoietic disorder. The expanded haematopoietic cells are also useful in the treatment of cyclic neutropenia, aplastic anaemia, thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome, systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome and myelofibrosis. The present sequence is an IL-3 mutant associated DNA sequence. Note: The present sequence is included in the sequence listing but is not mentioned anywhere else in the specification

Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,598-67	Length:	402
Score:	678.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.63%	Indels:	0
DB:	6	Gaps:	0

US-10-723-083-2 (1-142) x ABX00086 (1-402)

QY	15	MetAlaProAlaArgSerProSerThrGlnProTyrGluHisValAsnAlaIle	34
DB	1	ATGGCACCGGCTGCTCCCGTCTACCCAGCCCTGGGAACACGCTGAATGCCATC	60
QY	35	GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr	54
DB	61	CAGGAGGCCCGGCTGCTCCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACA	120
QY	55	ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu	74
DB	121	GTAGAAGTGATATCAGAAATGTTTACCTCCAGGAGCCGACTTGCCTCAGACCCGCTG	180
QY	75	GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet	94
DB	181	GAGCTGTACAAGCAGGGCTGCGGGCAGCCTCACCAGCTCAAGGGCCCCCTTGACCATG	240
QY	95	MetAlaSerHisTyrLysGlnHisCysProThrProGluThrSerCysAlaThrGln	114
DB	241	ATGGCCAGGCACCTACAAAGCAGCACTGCCCTCCAAACCCGGAACCTTCTCTGTGCAACCCAG	300
QY	115	IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe	134
DB	301	ATTATCACCTTTGAAAGTTTCAAGAGAACCTGGAAGGACTTCTCTGCTGTCATCCCTTT	360
QY	135	AspCysTyrGluProValGlnGlu	142
DB	361	GACTGCTGGAGCCAGTCCAGGAG	384
RESULT 11			
ID	ADJ14388		
XX	ADJ14388 standard; DNA; 402 BP.		
AC	ADJ14388;		
XX			
DT	20-MAY-2004 (first entry)		
XX			
DE	DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 151.		
XX	stem cell; antianaemic; immunostimulant; immunomodulator;		
KW	antiinflammatory; dermatological; immunosuppressive; cytostatic;		
KW	neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;		
KW	lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;		
KW	Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;		
KW	myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.		
XX	Unidentified.		
XX	US2003185790-A1.		
PN	02-OCT-2003.		
XX			
PF	26-FEB-2002; 2002US-00083446.		
XX			
PR	24-NOV-1992; 92US-00981044.		
PR	22-NOV-1993; 93WO-US011197.		
PR	04-FEB-1994; 94US-00192325.		
PR	02-FEB-1995; 95WO-US001185.		
PR	06-APR-1995; 95US-00411795.		
PR	06-JUN-1995; 95US-00446872.		
PR	09-DEC-1996; 96US-00762227.		
XX			
PA	(BAUE/) BAUER S C.		
PA	(ABRA/) ABRAMS M A.		
PA	(BRAF/) BRAFORD-GOLDBERG S R.		
PA	(CAFA/) CAPARON M H.		
PA	(EAST/) EASTON A M.		
PA	(KLEI/) KLEIN B K.		
PA	(MCKE/) MCKEARN J P.		
PA	(OLIN/) OLINS P O.		
PA	(PAIK/) PAIK K.		
PA	(THOM/) THOMAS J W.		
XX			

PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
 XX Klein BK, Mckearn JP, Olines PO, Paik K, Thomas JW;
 DR WPI; 2004-096775/10.
 XX
 XX Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
 PT aplastic anemia, involves culturing the stem cells with growth medium
 PT comprising chimera protein, and harvesting the cultured stem cells.
 XX
 XX Disclosure; SEQ ID NO 176; 202pp; English.
 XX
 XX The invention relates to a novel method whereby stem cells are ex vivo
 CC expanded via culturing the stem cells with a growth medium comprising a
 CC chimera protein, followed by harvesting of the cultured stem cells. The
 CC method of the invention has antianemic, immunostimulant,
 CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
 CC cytostatic and neuroprotective applications and may be useful to target
 CC hematopoietic cells for gene therapy, preferably for treating patients
 CC having a haemopoietic disorder characterised by decreased levels of
 CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
 CC system. The expanded ex vivo cells may be used to treat neutropenia,
 CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
 CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
 CC myelofibrosis. The current sequence is that of a DNA related to the human
 CC interleukin-3 (IL-3) mutant protein of the invention.
 XX
 SQ Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.59e-67 Length: 402
 Score: 678.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.63% Indels: 0
 DB: 12 Gaps: 0

US-10-723-083-2 (1-142) x ADJ14388 (1-402)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
 DB 1 ATGGCACCAGCTCGTTCCCGTCCCGTCTACCCAGCGGTGGGAACACAGTGAATGCCATC 60
 QY 35 GlnGluAlaArgGluLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
 DB 61 CAGGAGCCCGCGCTCTCTGAACTGAGTAGAGACACTGCTGAGATGAATGAACA 120
 QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
 DB 121 GTAGAAGTGAATATCAGAAATGTTTGACCTCCAGAGCCGACTTGCCTACAGCCCGCTG 180
 QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
 DB 181 GAGCTGTACAAGCAGGCGCTCGCGGCGAGCTCAACCAAGCTCAAGGCGCTTGACCATG 240
 QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
 DB 241 ATGGCCAGGCACATACAGCAGCAGCTGCCCTCCAAACCCCGGAACTTCCTGTGTCAACCCAG 300
 QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
 DB 301 ATTATCACCTTTGAAGATTTCAAAGAACCTGAGAGACTTCCTGTTGTATCCCTTT 360
 QY 135 AspCysTrpGluProValGlnGlu 142
 DB 361 GACTGTGGGAGCCAGTCCAGGAG 384
 RESULT 12
 AAN81322
 ID AAN81322 standard; DNA; 410 BP.
 XX
 AC AAN81322;
 XX
 XX 25-MAR-2003 (revised)

DT 06-JAN-1991 (first entry)
 XX
 DE Sequence (I) encoding human granulocyte macrophage colony stimulating
 XX factor (hGMCSF) with Ile at 101.
 DE
 XX Leukopenia therapy; bone marrow transplant; ds.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH complement(1..4)
 FT misc_feature /*tag= a
 FT /*note= "Sticky end"
 FT misc_feature complement(407..410)
 FT /*tag= b
 FT /*note= "Sticky end"
 XX
 PN JP63269983-A.
 XX
 PD 08-NOV-1988.
 XX
 XX 28-APR-1987; 87JP-00106148.
 PF
 XX 28-APR-1987; 87JP-00106148.
 PR
 XX (AMGE-) AMGEN.
 PA (KIRI) KIRIN BREWERY KK.
 XX
 XX WPI; 1988-358227/50.
 DR
 XX Human granulocyte macrophage colony stimulus factor prepn. - by forming
 PT plasmid contg. genetic information and Escherichia coli with the plasmid.
 XX
 PS Disclosure; Fig 7(1), Page 488; 17pp; Japanese.
 XX
 XX An expression plasmid contg. the DNA is prep'd. and used to transform
 CC E.coli. The transformant is cultured and hGMCSF is produced into the
 CC medium. hGMCSF stimulates the granulocyte macrophage system stem cell and
 CC promotes the formation of the granulocyte macrophage. hGMCSF is used in
 CC curing leukopenia caused by radiation therapy, or chemical therapy, or
 CC in promptly propagating leukocytes after bone marrow transplantation.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 410 BP; 109 A; 106 C; 91 G; 104 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.64e-67 Length: 410
 Score: 678.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.63% Indels: 0
 DB: 1 Gaps: 0

US-10-723-083-2 (1-142) x AAN81322 (1-410)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
 DB 11 ATGGCACCAGCTCGATCAGCTCCCGTCCACTCAACCATGGGAACATGTTAACGCAATC 70
 QY 35 GlnGluAlaArgGluLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
 DB 71 CAGGAAGCTCGCTGCTGCTGAACCTGCTCGGATGACTGCTGAAATGAACGAAACT 130
 QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
 DB 131 GTTGAAGTGAATCAGCAAAATGTTGATCTGCAGAACCCGACTTGTCTGCAAACCCGCTG 190
 QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
 DB 191 GAACTGTACAAACAGGCTCGCGTGGTTCTCTGACTAAACTGAAGAGTCCGCTGACTATG 250
 QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114

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Db      251 ATGGCTAGCCATTACAACAGCATTGTCCGCCGACTCCGAAACTTCTTGCTACTCAG 310
QY      115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
Db      311 ATCATCACTTTCGAATCTTTCAAGAAACCTGAAAGATTTCCTGCTGGTTATCCCGTTC 370
QY      135 AspCysTrpGluProValGlnGlu 142
Db      371 GATTGTTGGGACCGGTTCAAGAA 394

RESULT 13
AAN90383
ID      AAN90383 standard; DNA; 415 BP.
AC      AAN90383;
XX
DT      25-MAR-2003 (revised)
DT      01-NOV-1989 (first entry)
XX
DE      Synthetic gene for human granulocyte colony stimulating factor.
XX
KW      DNA; BspMI; restriction sites; blunt ends; fusion proteins;
KW      synthetic gene; human granulocyte colony stimulating factor.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key
FT      CDS
FT      14..397
FT      /*tag= a
XX
XX      GB2212160-A.
XX
XX      19-JUL-1989.
XX
XX      13-NOV-1987; 87GB-00726581.
XX
XX      13-NOV-1987; 87GB-00026581.
XX
XX      (BRBI-) BRITISH BIO-TECHN L.
XX
XX      Edwards RM;
XX
XX      WPI; 1989-208959/29.
XX      P-PSDB; AAP90118.
XX
XX      DNA including recognition site for BspMI enzyme - allowing generation of
XX      blunt end for fusion in prodn. of fusion proteins.
XX
XX      Disclosure; Fig 2; 23pp; English.
XX
XX      Synthetic gene for human granulocyte colony stimulating factor (GM-CSF)
XX      contg. useful restriction sites, and a BspMI site. See corresp. AAP90118.
XX      Useful for generating blunt ends in fusion protein prodn. (Updated on 25-
XX      MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
XX      CC field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 415 BP; 104 A; 130 C; 104 G; 77 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.67e-67 Length: 415
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 1 Gaps: 0

US-10-723-083-2 (1-142) x AAN90383 (1-415)

QY      15 MetaAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
Db      14 ATGGCACCCGCGGTTCACCCAGCCCGCAGCAGCAGCCCTGGGAGCATGTGATGCCAATC 73

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QY      35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
Db      74 CAGGAGCCCGCGGTCTCTGAACTGAGTACAGACACTGCTGCTGAGATGATGAACA 133
QY      55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db      134 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCTG 193
QY      75 GluLeuTyTrpLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db      194 GAGCTGTACAAGCAGGGCCTGCGGGCAGCCCTCACCAAGCTCAAGGGCCCCCTGACCATG 253
QY      95 MetAlaSerHisTyTrpLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db      254 ATGGCCAGCCACTACAGCAGCAGCTGCCCTCCAAACCCGGAACCTTCTGTGCAACCCAG 313
QY      115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
Db      314 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAAGGACTTCTGCTTGTCTATCCCTTT 373
QY      135 AspCysTrpGluProValGlnGlu 142
Db      374 GACTGCTGGGAGCCAGTCCAGGAG 397

RESULT 14
AAN90274
ID      AAN90274 standard; DNA; 415 BP.
AC      AAN90274;
XX
DT      25-MAR-2003 (revised)
DT      01-NOV-1989 (first entry)
XX
DE      Synthetic human granulocyte colony stimulating factor.
XX
KW      Synthetic DNA; human granulocyte colony stimulating factor;
KW      restriction sites; cassette mutagenesis; expression system.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key
FT      CDS
FT      14..397
FT      /*tag= a
XX
XX      GB2212159-A.
XX
XX      19-JUL-1989.
XX
XX      13-NOV-1987; 87GB-00026580.
XX
XX      13-NOV-1987; 87GB-00026580.
XX
XX      (BRBI-) BRITISH BIO-TECHN L.
XX
XX      Edwards RM;
XX
XX      WPI; 1989-208958/29.
XX      P-PSDB; AAP90115.
XX
XX      Human granulocyte-macrophage colony stimulating factor - synthetic DNA
XX      includes restriction sites for cassette mutagenesis and incorporation in
XX      expression systems.
XX
XX      Claim 2; Page 14 and fig 3a; 21pp; English.
XX
XX      Synthetic DNA encoding human granulocyte colony stimulating factor (GM-
XX      CSF), see corresp. AAP90115. Has useful restriction sites for: HindIII;
XX      BspMI; NcoI; BstIII; BsmI; EcoRV; BglI; ApaI; BclI; XbaI; BamHI; and
XX      EcoRI. Used to facilitate cassette mutagenesis of selected regions.
XX      Synthesised by phosphoramidite chemistry, by dividing desired gene into
XX      18 oligomers. (Updated on 25-MAR-2003 to correct PA field.)

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SQ Sequence 415 BP; 104 A; 130 C; 104 G; 77 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.67e-67 Length: 415
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 1 Gaps: 0

US-10-723-083-2 (1-142) x AAN90274 (1-415)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTTPGluHisValAsnAlaIle 34
DB 14 ATGGCACCCTGGTCTCCCTGAACCTGAGTAGACACTGCTGCTGAGATGAATGAACA 73
QY 35 GlnGluAlaArgGluLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 74 CAGGAGGCGCGGTCTCCCTGAACCTGAGTAGACACTGCTGCTGAGATGAATGAACA 133
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 134 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGACTTGCCTCAGACCCGCTG 193
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrIlysLeuLysGlyProLeuThrMet 94
DB 194 GAGCTGTACAAGCAGGCGCTGCGGGGAGCGCTCACCAGCTCAAGGGCCCCCTTGACCATG 253
QY 95 MetAlaSerHisTyrlsGlnHisCysProThrProGluThrSerCysAlaThrGln 114
DB 254 ATGGCCAGGCACCTACAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTGTGCAACCCAG 313
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
DB 314 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTGTGTCATCCCTTT 373
QY 135 AspCysTTPGluProValGlnGlu 142
DB 374 GACTGTGGAGCCAGTCCAGGAG 397

RESULT 15

AAQ97183
ID AAQ97183 standard; DNA; 822 BP.

XX AC AAQ97183;

XX DT 25-AUG-1999 (first entry)

XX DE PMON13035 DNA encoding IL-3 fusion protein.

XX Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09521254-A1.

XX PD 10-AUG-1995.

XX PF 02-FEB-1995; 95WO-US001185.

XX PR 04-FEB-1994; 94US-00192325.

XX PA (SEAR) SEARLE & CO G D.

XX PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;

XX PI Klein BK, McKearn JP, Olins PO, Paik K, Thomas JW;

XX DR WPI; 1995-283774/37.

XX DR P-PSDB; AAR79320.

XX PT Fusion proteins comprising a human interleukin-3 variant, a linker and

PT interleukin-3, a variant or a colony stimulating factor - useful to
PT increase haematopoietic cell prodn. in a mammal.

XX Claim 22; Page 167-168; 447pp; English.

XX A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC or IL-3 variant, and L is a linker. Genetic sequences are described in
CC AAW03235 - AAW03242, and specifically claimed examples are shown in
CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC recombinant DNA techniques. Specifically claimed examples of DNA
CC sequences (including the present sequence) which encode these proteins
CC are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
CC used to increase haematopoietic cell production. It is also useful as an
CC IL-3 antagonist or as a discrete antigenic fragment for production of
CC antibodies useful in immunoassays and immunotherapy. Antagonists are used
CC to block the growth of certain cancer cells and in treatment of asthma.
CC The fusion protein can also be used to stimulate bone marrow and blood
CC cell activation and growth in vitro before infusion; and to treat
CC diseases characterised by decreased levels of myeloid, erythroid,
CC lymphoid and/or megakaryocyte cells of the haematopoietic system. The
CC protein has the usual activity of both its component proteins, but may
CC have increased synergistic activity and reduced undesired side effects
XX SQ Sequence 822 BP; 222 A; 244 C; 180 G; 176 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.25e-67 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 2 Gaps: 0

US-10-723-083-2 (1-142) x AAQ97183 (1-822)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTTPGluHisValAsnAlaIle 34
DB 439 ATGGCACCCTGGTCTCCCTGAACCTGAGTAGACACTGCTGCTGAGATGAATGAACA 498
QY 35 GlnGluAlaArgGluLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 499 CAGGAGGCGCGGTCTCCCTGAACCTGAGTAGACACTGCTGCTGAGATGAATGAACA 558
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 559 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGGACTTGCCTCAGACCCGCTG 618
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 619 GAGCTGTACAAGCAGGCGCTGCGGGGAGCGCTCACCAGCTCAAGGGCCCCCTTGACCATG 678
QY 95 MetAlaSerHisTyrlsGlnHisCysProThrProGluThrSerCysAlaThrGln 114
DB 679 ATGGCAGGCACCTACAAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTGTGCAACCCAG 738
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
DB 739 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTGTGTCATCCCTTT 798
QY 135 AspCysTTPGluProValGlnGlu 142
DB 799 GACTGTGGAGCCAGTCCAGGAG 822

Search completed: March 11, 2005, 18:36:51
Job time : 480 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 17:26:51 ; Search time 3628 Seconds
(without alignments)
1896.538 Million cell updates/sec

Title: US-10-723-083-2

Perfect score: 765

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	682	89.2	777	6 AR202206	AR202206 Sequence
2	682	89.2	777	6 AR223208	AR223208 Sequence
3	678	88.6	384	6 E11629	E11629 hgm-CSP-enc
4	678	88.6	402	6 AR202280	AR202280 Sequence

5	678	88.6	402	6	AR223282	AR223282 Sequence
6	678	88.6	415	6	A00367	A00367 Artificial
c 7	678	88.6	415	6	A00368	A00368 Artificial
8	678	88.6	415	6	A14305	A14305 GM-CSF gene
c 9	678	88.6	415	6	A14306	A14306 GM-CSF gene
10	678	88.6	822	6	AR202220	AR202220 Sequence
11	678	88.6	822	6	AR223222	AR223222 Sequence
12	678	88.6	903	6	AR202217	AR202217 Sequence
13	678	88.6	903	6	AR223219	AR223219 Sequence
14	676	88.4	1630	6	BD222938	BD222938 Heteromim
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16	673	88.0	384	6	A20082	A20082 Pcti-Hind I
17	673	88.0	384	6	E11628	E11628 hgm-CSP-enc
c 18	673	88.0	392	6	A20083	A20083 Pcti-Hind I
19	673	88.0	392	6	I49837	I49837 Sequence 1
20	673	88.0	418	6	A11762	A11762 Artificial
c 21	673	88.0	418	6	A11763	A11763 Artificial
22	673	88.0	435	6	CQ834914	CQ834914 Sequence
23	673	88.0	435	6	CQ834915	CQ834915 Sequence
24	673	88.0	435	6	ARS33388	ARS33388 Sequence
25	673	88.0	435	6	BD105958	BD105958 Animal mo
26	673	88.0	436	6	E01740	E01740 gene encodi
27	673	88.0	505	6	I08646	I08646 Sequence 3
28	673	88.0	505	9	HUMCSFGMB	M11734 Human granu
29	673	88.0	644	6	E01141	E01141 cDNA encodi
30	673	88.0	660	6	AR364645	AR364645 Sequence
31	673	88.0	661	6	E00951	E00951 cDNA encodi
32	673	88.0	661	6	I04859	I04859 Sequence 3
33	673	88.0	661	6	AR363793	AR363793 Sequence
34	673	88.0	756	6	CQ721607	CQ721607 Sequence
35	673	88.0	756	6	CQ803372	CQ803372 Sequence
36	673	88.0	763	6	E02287	E02287 DNA encodin
37	673	88.0	787	6	I08093	I08093 Sequence 1
38	673	88.0	787	6	I08094	I08094 Sequence 1
39	673	88.0	787	6	I08401	I08401 Sequence 1
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41	673	88.0	787	6	I09160	I09160 Sequence 21
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43	673	88.0	896	6	A20086	A20086 BamHI-HindI
c 44	673	88.0	896	6	A20087	A20087 BamHI-HindI
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ALIGNMENTS

RESULT 1
AR202206
LOCUS AR202206
DEFINITION Sequence 55 from patent US 6361977.
ACCESSION AR202206
VERSION AR202206.1 GI:20256745
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 777)
AUTHORS Bauer, S. Christopher., Abrams, M. Allen., Braford-Goldberg, S. Ruth., Caparon, M. Helena., Easton, A. Michael., Klein, B. Kure., McKearn, J. P., Olin, P. O., Paik, K. and Thomas, J. W.
TITLE Methods of using multivalent IL-3 hematopoiesis fusion protein
JOURNAL Patent: US 6361977-A 55 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..777
/organism="unknown"
/mol_type="unassigned DNA"

linear PAT 20-APR-2002

Alignment Scores:
Pred. No.: 9.49e-60 Length: 777
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Best Local Similarity: 97.01% Mismatches: 4
Query Match: 89.15% Indels: 0

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DB: 6 Gaps: 0
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QY 29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
Db 436 GAACAGTGAATGCCATCCAGAGGCGCGGCTCTCTGAACTGAGTAGACACTGCT 495
QY 49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnProTrp 68
Db 496 GCTCAGATGAATGAAACAGTAGAAGTATCAGAAATGTTTGACCTCCAGAGCGGACT 555
QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
Db 556 TGCCTACAGACCGCGCTGGAGCTGTACAGCAGGCGCTCGCGGGCAGCCTCACCAGCTC 615
QY 89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
Db 616 AAGGGCCCCCTTGACCATGATGCCAGCCACTACAAGCAGACTGCCCTCCAAACCCGGAA 675
QY 109 ThrSerCysAlaThrGlnIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
Db 676 ACTTCTGTGCAACCCAGATTATCACCCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735
QY 129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
Db 736 CTGCTGTGTCATCCCTTTGACTGCTGGAGCCAGTCCAGAG 777

RESULT 3
E11629
LOCUS hgm-CSF-encoding DNA for efficient expression in E.coli. 384 bp DNA linear PAT 29-SEP-1997
DEFINITION hgm-CSF-encoding DNA for efficient expression in E.coli.
ACCESSION E11629
VERSION E11629.1 GI:22025265
KEYWORDS JP 1996173185-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 384)
AUTHORS Matsuki,S., Ozawa,T. and Tamai,Y.
TITLE PRODUCTION OF STIMULATING FACTOR FOR HUMAN GRANULOCYTTIC MACROPHAGE COLONY
JOURNAL Patent: JP 1996173185-A 2 09-JUL-1996;
COMMENT AMGEN, KIRIN BREWERY CO LTD
OS None
OC Artificial sequences.
PN JP 1996173185-A/2
PD 09-JUL-1996
PF 28-APR-1987 JP 1995263370
PI MATSUKI SHIGERU, OZAWA TADASHI, TAMAI YUKIO
PC C12P21/02,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),(C12N1/21,
CC strandedness: Double;
CC topology: Linear;
CC Key Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0

US-10-723-083-2 (1-142) x E11629 (1-384)
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Db 241 ATGGCTAGCATTAACAACAGCATTCGCCGACTCCGAAACTCTTGTGCTACTCAG 300
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Qy 135 AspCysTrpGluProValGlnGlu 142
Db 361 GATTGTTGGGAACCGGTTCAGGAA 384
RESULT 4
LOCUS AR202280 402 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 176 from patent US 6361977.
ACCESSION AR202280
VERSION AR202280.1 GI:20256819
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Bauer, S., Christopher., Abrams, M., Allen., Braford-Goldberg, S., Ruth.,
Caparon, M., Helena., Easton, A., Michael., Klein, B., Kure., McKearn, J. P.,
Olin, P. O., Paik, K. and Thomas, J. W.
TITLE Methods of using multivariant IL-3 hematopoiesis fusion protein
JOURNAL Patent: US 6361977-A 176 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..402
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/mol_type="unassigned DNA"
ORIGIN
Alignment Scores: 1.12e-59 Length: 402
Pred. No.: 678.00 Matches: 128
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 88.63% Indels: 0
Query Match: 6 Gaps: 0
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Qy 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db 61 CAGGAGCCCGCGCTCTCTGAAACCTGAGTAGACACTGCTGCTGAGATGAATGAACA 120
Qy 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db 121 GTAGAAGTGATATCAGAAATGTTGACCTCCAGAGCCGACTTGCCTACAGACCCGCTG 180
Qy 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 181 GAGCTGTACAAGCAGGCGCTGCGGGCAGCCTCACCAGCTCAAGGCGCCCTTGACCATG 240
Qy 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 241 ATGGCCAGCCACTACAAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCCTGCTGCAACCCAG 300
Qy 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
Db 301 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTTGTGTCATCCCTTT 360
Qy 135 AspCysTrpGluProValGlnGlu 142
Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384
RESULT 6
LOCUS A00367 415 bp DNA linear PAT 09-MAR-1993
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Qy 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
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Qy 135 AspCysTrpGluProValGlnGlu 142
Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384
RESULT 5
LOCUS AR223282 402 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 176 from patent US 6436387.
ACCESSION AR223282
VERSION AR223282.1 GI:23331290
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Bauer, S. C., Abrams, M. A., Braford-Goldberg, S. R., Caparon, M. H.,
Easton, A. M., Klein, B. K., McKearn, J. P., Olin, P. O., Paik, K. and
Thomas, J. W.
TITLE Methods of ex-vivo expansion of hematopoietic cells using
multivariant IL-3 hematopoiesis chimera proteins
JOURNAL Patent: US 6436387-A 176 20-AUG-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Pred. No.: 678.00 Matches: 128
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 88.63% Indels: 0
Query Match: 6 Gaps: 0
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Qy 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
Db 1 ATGGCAACCGCTGCTGTTCCCGCTCTACCCAGCCGTGGGAACACGTAATGCCATC 60
Qy 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
Db 61 CAGGAGCCCGCGCTCTCTGAAACCTGAGTAGACACTGCTGCTGAGATGAATGAACA 120
Qy 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db 121 GTAGAAGTGATATCAGAAATGTTGACCTCCAGAGCCGACTTGCCTACAGACCCGCTG 180
Qy 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 181 GAGCTGTACAAGCAGGCGCTGCGGGCAGCCTCACCAGCTCAAGGCGCCCTTGACCATG 240
Qy 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 241 ATGGCCAGCCACTACAAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCCTGCTGCAACCCAG 300
Qy 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
Db 301 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTTGTGTCATCCCTTT 360
Qy 135 AspCysTrpGluProValGlnGlu 142
Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384
RESULT 6
LOCUS A00367 415 bp DNA linear PAT 09-MAR-1993
```

DEFINITION Artificial gene for granulocyte/macrophage colony stimulating factor.

ACCESSION A00367

VERSION A00367.1 GI:344179

KEYWORDS granulocyte-macrophage colony stimulating factor; synthetic gene.

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 415)

AUTHORS Synthetic-gene

TITLE Patent: GB 2212159-A 2 19-JUL-1989;

JOURNAL Location/Qualifiers

FEATURES source

1..415

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

CDS

14..400

/notes="synthetic"

/codon_start=1

/transl_table=11

/product="granulocyte/macrophage colony stimulating factor"

/protein_id="CAA00057.1"

/db_xref="GI:344180"

/translation="MAPARSPSPSTQPEWHVNAIQBARLLNLSRDYTAEMNETVEVISMFDIQEPTCLQTRLELYKGLRSLTKLKGPLTMWASHYKHCPPTPETSCATQIITFESFENLKDFLLVFPDCWEPVQE"

ORIGIN

Alignment Scores:

Pred. No.: 1.16e-59 Length: 415

Score: 678.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.63% Indels: 0

DB: 6 Gaps: 0

US-10-723-083-2 (i-142) x A00367 (1-415)

QY 15 MetAlaProAlaArgSerProSerThrGlnProThrGluHisValAsnAlaIle 34

14 ATGGCACCCCGCGGTCTCCTGAACCTGAGTACAGACACTTGCCTGAGATGATGCCATC 73

QY 35 GlnGluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54

74 CAGGAGCGCGCGGTCTCCTGAACCTGAGTACAGACACTTGCCTGAGATGATGCCATC 133

QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74

134 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCGGACTTGCCTACAGACCGCGCTG 193

QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94

194 GAGCTGTACAGCAGGCGCTTGGGGCAGCGCTCACCAAGCTCAGGGCCCCCTTGACCATG 253

QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114

254 ATGGCCAGCAGCACTACAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTGTGCAACCCAG 313

QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134

314 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTGTGTCATCCCTTT 373

QY 135 AspCysTrpGluProValGlnGlu 142

374 GACTGCTGGAGCCAGTCCAGGAG 397

RESULT 7

A00368/c

LOCUS Artificial gene for granulocyte/macrophage colony stimulating factor, reverse complement.

DEFINITION Artificial gene for granulocyte/macrophage colony stimulating factor.

ACCESSION A00368

VERSION A00368.1 GI:344181

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 415)

AUTHORS Synthetic-gene

TITLE Patent: GB 2212159-A 3 19-JUL-1989;

JOURNAL Location/Qualifiers

FEATURES source

1..415

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.: 1.16e-59 Length: 415

Score: 678.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.63% Indels: 0

DB: 6 Gaps: 0

US-10-723-083-2 (1-142) x A00368 (1-415)

QY 15 MetAlaProAlaArgSerProSerThrGlnProThrGluHisValAsnAlaIle 34

402 ATGGCACCCCGCGGTCTCCTGAACCTGAGTACAGACACTTGCCTGAGATGATGCCATC 343

QY 35 GlnGluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54

342 CAGGAGCGCGCGGTCTCCTGAACCTGAGTACAGACACTTGCCTGAGATGATGCCATC 283

QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74

282 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCGGACTTGCCTACAGACCGCGCTG 223

QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94

222 GAGCTGTACAGCAGGCGCTTGGGGCAGCGCTCACCAAGCTCAGGGCCCCCTTGACCATG 163

QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114

162 ATGGCCAGCAGCACTACAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTGTGCAACCCAG 103

QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134

102 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTGTGTCATCCCTTT 43

QY 135 AspCysTrpGluProValGlnGlu 142

42 GACTGCTGGAGCCAGTCCAGGAG 19

RESULT 8

A14305

LOCUS GM-CSF gene (from Homo sapiens).

DEFINITION GM-CSF gene (from Homo sapiens).

ACCESSION A14305

VERSION A14305.1 GI:491775

KEYWORDS synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 415)

AUTHORS DNA sequence

TITLE Patent: GB 2212160-A 2 19-JUL-1989;

JOURNAL Location/Qualifiers

FEATURES source

1..415

/organism="synthetic construct"

/mol_type="unassigned DNA"

gene /db_xref="taxon:32630"
14..400
/genes="human GM-CSF gene"
CDS 14..400
/genes="human GM-CSF gene"
/codon_start=1
/transl_table=11
/protein_id="CAA01150.1"
/db_xref="GI:491776"
/translation="NAPARSPSPSTQPEWHVNAIQBARLLNLSRDTAAEMNETVEVI
SMFLOQETCLQRLKLYKGLRSLTKLKGPLTMASHYKHCPPTPETSCATQII
TFESFENLKDPLLVIIPDCWBPQV"

ORIGIN

Alignment Scores:
Pred. No.: 1.16e-59 Length: 415
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0

US-10-723-083-2 (1-142) x A14306 (1-415)

QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTTPGluHisValAenAlaIle 34
DB 14 ATGGCACCCTGGGCTCTCTGAACTGAGTACAGACCTGCTGCTGAGATGAATGCAATC 73
QY 35 GlnGluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAenGluThr 54
DB 74 CAGGAGCCCGCGCTCTCTGAACTGAGTACAGACCTGCTGCTGAGATGAATGAACA 133
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 134 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCCGACTTGCCTCAGACCCGCTG 193
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 194 GAGCTGTACAAGCAGGCGCTCGGGGCGAGCTCACCAGCTCAAGGGCCCTTGACCATG 253
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 254 ATGGCCAGCCACTACAGCAGACTGCTCTCCAAACCCCGGAACTTCTTGTGCAACCCAG 313
QY 115 IleIleThrPheGluSerPheLysGluAenLeuLysAspPheLeuLeuValIleProPhe 134
DB 314 ATTATCACCTTTGAAAGTTTCAAGAGAACTTGAAGGACTTCTGCTTGTCTATCCCTTT 373
QY 135 AspCysTTPGluProValGlnGlu 142
DB 374 GACTGCTGGAGCCAGTCCAGGAG 397

RESULT 9
A14306/C
LOCUS A14306 415 bp DNA linear PAT 18-JAN-1994
DEFINITION GM-CSF gene (from Homo sapiens).
ACCESSION A14306
VERSION A14306.1 GI:489685

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 415)
AUTHORS other sequences; artificial sequences.
TITLE DNA sequence
JOURNAL Patent: GB 2212160-A 3 19-JUL-1989;
FEATURES Location/Qualifiers
source 1..415
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores:

Pred. No.: 1.16e-59 Length: 415
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0

US-10-723-083-2 (1-142) x A14306 (1-415)

QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTTPGluHisValAenAlaIle 34
DB 402 ATGGCACCCTGGGCTCTCTGAACTGAGTACAGACCTGCTGCTGAGATGAATGCAATC 343
QY 35 GlnGluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAenGluThr 54
DB 342 CAGGAGCCCGCGCTCTCTGAACTGAGTACAGACCTGCTGCTGAGATGAATGAACA 283
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 282 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCCGACTTGCCTCAGACCCGCTG 223
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 222 GAGCTGTACAAGCAGGCGCTCGGGGCGAGCTCACCAGCTCAAGGGCCCTTGACCATG 163
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 162 ATGGCCAGCCACTACAGCAGCAGCTGCTCTCCAAACCCCGGAACTTCTTGTGCAACCCAG 103
QY 115 IleIleThrPheGluSerPheLysGluAenLeuLysAspPheLeuLeuValIleProPhe 134
DB 102 ATTATCACCTTTGAAAGTTTCAAGAGAACTTGAAGGACTTCTGCTTGTCTATCCCTTT 43
QY 135 AspCysTTPGluProValGlnGlu 142
DB 42 GACTGCTGGAGCCAGTCCAGGAG 19

RESULT 10

AR202220
LOCUS AR202220 822 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 69 from patent US 6361977.
ACCESSION AR202220
VERSION AR202220.1 GI:20256759

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 822)
AUTHORS Bauer, S. Christopher., Abrams, M. Allen., Braford-Goldberg, S. Ruth.,
Caparon, M. Helena., Easton, A. Michael., Klein, B. Kure., McKearn, J. P.,
Olin, P. O., Paik, K. and Thomas, J. W.
TITLE Methods of using multivalent IL-3 hematopoiesis fusion protein
JOURNAL Patent: US 6361977-A 69 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..822
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.58e-59 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0

US-10-723-083-2 (1-142) x AR202220 (1-822)

QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTTPGluHisValAenAlaIle 34
DB 439 ATGGCACCCTGGGCTCTCTGAACTGAGTACAGACCTGCTGCTGAGATGAATGCAATC 498

QY 35 GlnGluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
|
|
|
Db 499 CAGGAGCCCGCGTCTCTCGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACA 558
|
|
|
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
|
|
|
Db 559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTCAGACCCGCGCTG 618
|
|
|
QY 75 GluLeuTyrlYsGlnGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
|
|
|
Db 619 GAGCTGTACAGCAGCGCTCGCGGCGAGCTCACCAGCTCAAGGGCCCCCTTGACCATG 678
|
|
|
QY 95 MetAlaSerHisTyrlYsGlnHisCysProThrProGluThrSerCysAlaThrGln 114
|
|
|
Db 679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAAACCCCGGAACTTCTCTGTGCAACCCAG 738
|
|
|
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
|
|
|
Db 739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCTGCTTGTCTATCCCTTT 798
|
|
|
QY 135 AspCysTrpGluProValGlnGlu 142
|
|
|
Db 799 GACTGTGGAGCCAGTCCAGGAG 822
|
|
|
RESULT 11
AR223222
LOCUS AR223222 822 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 69 from patent US 6436387.
ACCESSION AR223222
VERSION AR223222.1 GI:23331230
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 822)
AUTHORS Bauer, S.C., Abrams, M.A., Braford-Goldberg, S.R., Caparon, M.H., Easton, A.M., Klein, B.K., McKearn, J.P., Olin, P.O., Paik, K. and Thomas, J.W.
TITLE Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoiesis chimera proteins
JOURNAL Patent: US 6436387-A 69 20-AUG-2002;
FEATURES Location/Qualifiers
source
1..822
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2,58e-59 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0
US-10-723-083-2 (1-142) x AR223222 (1-822)
QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
|
|
|
Db 439 ATGGCACCAGCTGCTCTCCCGTCCCGCTACCCAGCGCTGGGAACAGTGAATGCCATC 498
|
|
|
QY 35 GlnGluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
|
|
|
Db 499 CAGGAGCCCGCGTCTCTCGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACA 558
|
|
|
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
|
|
|
Db 559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTCAGACCCGCGCTG 618
|
|
|
QY 75 GluLeuTyrlYsGlnGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
|
|
|
Db 619 GAGCTGTACAGCAGCGCTCGCGGCGAGCTCACCAGCTCAAGGGCCCCCTTGACCATG 678

QY 95 MetAlaSerHisTyrlYsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
|
|
|
Db 679 ATGGCAGCCACTACAAGCAGCACTGCCCTCCAAACCCCGGAACTTCTCTGTGCAACCCAG 738
|
|
|
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
|
|
|
Db 739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCTGCTTGTCTATCCCTTT 798
|
|
|
QY 135 AspCysTrpGluProValGlnGlu 142
|
|
|
Db 799 GACTGTGGAGCCAGTCCAGGAG 822
|
|
|
RESULT 12
AR202217
LOCUS AR202217 903 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 66 from patent US 6361977.
ACCESSION AR202217
VERSION AR202217.1 GI:20256756
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 903)
AUTHORS Bauer, S.Christopher., Abrams, M.Allen., Braford-Goldberg, S.Ruth., Caparon, M.Helena., Easton, A.Michael., Klein, B.Kure., McKearn, J.P., Olin, P.O., Paik, K. and Thomas, J.W.
TITLE Methods of using multivariant IL-3 hematopoiesis fusion protein
JOURNAL Patent: US 6361977-A 66 26-MAR-2002;
FEATURES Location/Qualifiers
source
1..903
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2,87e-59 Length: 903
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0
US-10-723-083-2 (1-142) x AR202217 (1-903)
QY 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
|
|
|
Db 520 ATGGCACCAGCTGCTCTCCCGTCCCGCTACCCAGCGCTGGGAACAGTGAATGCCATC 579
|
|
|
QY 35 GlnGluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
|
|
|
Db 580 CAGGAGCCCGCGTCTCTCGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACA 639
|
|
|
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
|
|
|
Db 640 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTCAGACCCGCGCTG 699
|
|
|
QY 75 GluLeuTyrlYsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
|
|
|
Db 700 GAGCTGTACAGCAGCGCTCGCGGCGAGCTCACCAGCTCAAGGGCCCCCTTGACCATG 759
|
|
|
QY 95 MetAlaSerHisTyrlYsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
|
|
|
Db 760 ATGGCAGCCACTACAAGCAGCACTGCCCTCCAAACCCCGGAACTTCTCTGTGCAACCCAG 819
|
|
|
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
|
|
|
Db 820 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCTGCTTGTCTATCCCTTT 879
|
|
|
QY 135 AspCysTrpGluProValGlnGlu 142
|
|
|
Db 880 GACTGTGGAGCCAGTCCAGGAG 903

```

RESULT 13
LOCUS AR223219 903 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 66 from patent US 6436387.
ACCESSION AR223219
VERSION AR223219.1 GI:23331227
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 903)
AUTHORS Bauer, S.C., Abrams, M.A., Braford-Goldberg, S.R., Caparon, M.H.,
Easton, A.M., Klein, B.K., McKearn, J.P., Olin, P.O., Paik, K. and
Thomas, J.W.
TITLE Methods of ex-vivo expansion of hematopoietic cells using
multivariant IL-3 hematopoiesis chimera proteins
JOURNAL Patent: US 6436387-A 66 20-AUG-2002;
FEATURES
source
1..903
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2,87e-59 Length: 903
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 6 Gaps: 0
US-10-723-083-2 (1-142) x AR223219 (1-903)
QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
Db 520 ATGGCACCGGCTGTTCCCGTCCCGTCTACCCAGCGCTGGGAACACGTGATGCATC 579
QY 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
Db 580 CAGGAGGCGCGGCTCTCTGAAACCTGAGTAGAGACACTGCTGCTGAGATGAACA 639
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db 640 GTAGAAGTGAATACAGAAATGTTTGACCTCCAGAGCCGACTTGCCTACAGACCCCTG 699
QY 75 GluLeuTyrllysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 700 GAGCTGTACAGCAGGCGCTCGGGGCGAGCTCACCAGCTCAAGGGCCCTTGACCATG 759
QY 95 MetAlaSerHisTyrllysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 760 ATGGCCAGCCACTACAAAGCAGCAGCTGCGCTCCCAACCCCGGAAACTTCCTGTGCAACCCAG 819
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
Db 820 ATTATCACCTTTGAAAGTTTCAAGAGAACTCAAGAGACTTCCTGCTGTGTCATCCCTTT 879
QY 135 AspCysTrpGluProValGlnGlu 142
Db 880 GACTGTGGGAGCCAGTCCAGGAG 903
RESULT 14
LOCUS BD222938 1630 bp DNA linear PAT 17-JUL-2003
DEFINITION Heterominitobodies.
ACCESSION BD222938
VERSION BD222938.1 GI:33032708
KEYWORDS JP 2002521053-A/32.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1630)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1630)
AUTHORS Kufer, P., Dreier, T., Baeuerle, P.A., Borschert, K. and Zettl, F.
TITLE Heterominitobodies
JOURNAL Patent: JP 2002521053-A 32 16-JUL-2002;
COMMENT MICROMET AG
OS Homo sapiens (human)
PN JP 2002521053-A/32
PD 16-JUL-2002
PF 28-JUL-1999 JP 2000562401
PR 28-JUL-1998 EP 98114082.5
PI PETER KUFER, TORSTEN DREIER, PATRICK A BAEUERLE, KATRIN
BORSCHERT.
PI FLORIAN ZETTL
PC C12N15/09, A61K35/76, A61K38/00, A61K38/21, A61P35/00, A61P35/02,
PC C07K19/00,
PC C12N5/10, C12P21/02, G01N33/53, G01N33/53// (C12N5/10, C12R1:91),
PC (C12P21/02, C12R1:91), C12N15/00, C12N5/00, A61K37/02, A61K37/66,
PC (C12N5/00, C12R1:91)
CC Heterominitobodies
FH Key Location/Qualifiers
FT CDS
1..1630
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 9,1e-59 Length: 1630
Score: 676.00 Matches: 128
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 2
Query Match: 88.37% Indels: 0
DB: 6 Gaps: 0
US-10-723-083-2 (1-142) x BD222938 (1-1630)
QY 13 GlyArgMetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsn 32
Db 1200 GGTGGGTCCGACCCCGCGCTCGCCAGCCGCGAGCAGCCCTGGGAGCATGTGAAT 1259
QY 33 AlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsn 52
Db 1260 GCATCTCAGAGGCGCGGCTCTCTGAAACCTGAGTAGAGACACTGCTGCTGAGATGAAT 1319
QY 53 GluThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThr 72
Db 1320 GAAACAGTAGAGTCACTCAGAAATGTTTGACCTCCAGAGCCGAGCTGCTACAGACC 1379
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ACCESSION AX023365
VERSION AX023365.1 GI:10183777
KEYWORDS

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Job time : 3634 secs

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Homo sapiens (human)

Homo sapiens

Kufer, P., Zettl, F., Dreier, T., Baeuerle, P. A. and Borschert, K.

Heteromimibodies

Patent: WO 006605-A 36 10-FEB-2000;

KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;

BAEUEERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER

BIOMEDIZINIS (DE)

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Pred. No.:

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Percent Similarity:

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GenCore version 5.1.6
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Run on: March 11, 2005, 18:21:21 ; Search time 163 Seconds
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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	682	89.2	777	3	US-08-446-872A-55
5	682	89.2	777	5	US-08-762-227A-55
6	682	89.2	777	5	PCT-US95-01185-55
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					Sequence 69, Appl

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23	673	88.0	435	4	US-09-826-025-8	Sequence 8, Appl
24	673	88.0	435	4	US-10-188-056-31	Sequence 31, Appl
25	673	88.0	435	4	US-10-188-056-32	Sequence 32, Appl
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ALIGNMENTS

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; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
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; APPLICATION NUMBER: 08/446,872
; FILING DATE:
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-318-55

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Best Local Similarity: 97.01% Mismatches: 4
Query Match: 89.15% Indels: 0

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; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 737-6986
; TELEFAX: (314) 737-6972
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-468-609A-55
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; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; TITLE OF INVENTION: Fusion Protein
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.,
; STREET: P. O. Box 5110
; CITY: Chicago

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; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/446,872A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; NAME: Bennett, Dennis A.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-446-872A-55

Alignment Scores:
Pred. No.: 1.89e-76 Length: 777
Score: 682.00 Matches: 130
Percent Similarity: 97.01% Conservative: 0
Best Local Similarity: 97.01% Mismatches: 4
Query Match: 89.15% Indels: 0
DB: 3 Gaps: 0

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; Patent No. 6436387

GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Ollins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESS: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-8881
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-08-762-227A-55

Alignment Scores:
Pred. No.: 1.89e-76 Length: 777
Score: 682.00 Matches: 130
Percent Similarity: 97.01% Conservative: 0
Best Local Similarity: 97.01% Mismatches: 4
Query Match: 89.15% Indels: 0
DB: 3 Gaps: 0

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; Patent No. 6436387
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QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
Db 556 TGCTACAGACCCGCTGGAGCTGTACACAGAGGCTCGGGGCGAGCCTCACCAAGCTC 615
QY 89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
Db 616 AAGGGCCCTTGACCATGATGGCCAGCCACTACAGCAGCAGCTGCCCTCCAAACCCCGAA 675
QY 109 ThrSerCysAlaThrGlnIleThrPheGluSerPheLysGluLeuLeuLysAspPhe 128
Db 676 ACTTCCTGTCAACCCAGATTATCACCTTTGAAGTTTCAAGAGAACCTGAAGGACTTC 735
QY 129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
Db 736 CTGCTGTGATCCCTTTGACTGCTGGAGCCAGTCCAGGAG 777
RESULT 5
PCT-US95-01185-55
; Sequence 55, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 02-FEB-1995
; APPLICATION NUMBER: PCT/US95/01185
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192325
; FILING DATE: 14-FEB-1994
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-55
Alignment Scores:
Pred. No.: 1.89e-76 Length: 777
Score: 682.00 Matches: 130
Percent Similarity: 97.01% Conservative: 0
Best Local Similarity: 97.01% Mismatches: 4
Query Match: 89.15% Indels: 0
DB: 5 Gaps: 0
US-10-723-083-2 (1-142) x PCT-US95-01185-55 (1-777)
QY 9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProThrGlnProTrp 28
Db 376 TCTGGCGGCGCTCCAACTGGCACCGCTCGTTCCCGCTCCCGCTACCCAGCGCTGG 435
QY 29 GluHisValAsnAlaIleGlnAlaArgLeuLeuAsnLeuSerArgAspThrAla 48
Db 436 GAACAGCTGAATGCCATCCAGAGGCGCGCGCTCTCTGAACCTGAGTAGACACTGCT 495
QY 49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnProThr 68
Db 496 GCTGAGATGAATGAACAGTAGAGTATCAGAAATGTTTACCTCCAGGAGCGGACT 555
QY 69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
Db 556 TGCTACAGACCCGCTGGAGCTGTACAGCAGGCGCTCGGGGCGAGCCTCACCAAGCTC 615

QY 89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
Db 616 AAGGGCCCTTGACCATGATGGCCAGCCACTACAGCAGCAGCTGCCCTCCAAACCCCGAA 675
QY 109 ThrSerCysAlaThrGlnIleThrPheGluSerPheLysGluLeuLeuLysAspPhe 128
Db 676 ACTTCCTGTCAACCCAGATTATCACCTTTGAAGTTTCAAGAGAACCTGAAGGACTTC 735
QY 129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
Db 736 CTGCTGTGATCCCTTTGACTGCTGGAGCCAGTCCAGGAG 777
RESULT 6
US-08-469-318-176
; Sequence 176, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-318-176
Alignment Scores:
Pred. No.: 2.23e-76 Length: 402
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 3 Gaps: 0
US-10-723-083-2 (1-142) x US-08-469-318-176 (1-402)
QY 15 MetalProAlaArgSerProSerProThrGlnProTrpGluHisValAsnAlaIle 34
Db 1 ATGGCACCGGCTCGTTCCCGCTCCCGCTACCCAGCGTGGGACACGTAATCCCATC 60
QY 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
Db 61 CAGGAGGCGCGGCTCTCTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACA 120
QY 55 ValGluValIleSerGluMetPheAspLeuGlnProThrCysLeuGlnThrArgLeu 74
Db 121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCGGACTTGCCTACAGACCCGCTG 180
QY 75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 181 GAGCTGTAAAGCAGGCGCTCGGGGCGAGCTTCACCAAGCTCAAGGGCCCTTGACCATG 240
QY 95 MetalSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 241 ATGGCAGCCACTACAGCAGCAGCTGCCCTCCAAACCCCGGAAACTTCTGTGTCAACCCAG 300
QY 115 IleIleThrPheGluSerPheLysGluLeuLeuLysAspPheLeuLeuValIleProPhe 134

Db 301 ATTATCACCTTTGAAGATTTCAGAGAACCTCGAGACTTCTGCTGTGTCATCCCTTT 360
|||||

QY 135 AspCysTrpGluProValGlnGlu 142
|||||

Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384
|||||

RESULT 7

US-08-468-609A-176

; Sequence 176, Application US/08468609A

; Patent No. 6030812

; GENERAL INFORMATION:

; APPLICANT: Abrams, Mark A.

; APPLICANT: Bauer, S. C.

; APPLICANT: Braford-Goldberg, Sarah R.

; APPLICANT: Caparon, Mairé H.

; APPLICANT: Easton, Alan M.

; APPLICANT: Klein, Barbara K.

; APPLICANT: McKearn, John P.

; APPLICANT: Olin, Peter O.

; APPLICANT: Paik, Kumnan

; APPLICANT: Thomas, John W.

; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-

; NUMBER OF SEQUENCES: 197

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,

; ADDRESSEE: Corporate Patent Dept.

; STREET: P. O. Box 5110

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60680

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,609A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/192,325

; FILING DATE: 14-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bennett, Dennis A.

; REGISTRATION NUMBER: 34,547

; REFERENCE/DOCKET NUMBER: C-2790/3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314)737-6986

; TELEFAX: (314)737-6972

; INFORMATION FOR SEQ ID NO: 176:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-468-609A-176

Alignment Scores:

Pred. No.: 2,23e-76

Score: 678.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 88.63%

DB: 3

Length: 402

Matches: 128

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-723-083-2 (1-142) x US-08-468-609A-176 (1-402)

QY 15 MetAlaProAlaArgSerProSerThrGlnProThrGluHisValAlaLeu 34

|||||

Db 1 ATGGCACCGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 60

QY 35 GlnGluAlaArgSerArgSerLeuSerArgSerThrAlaAlaGluMetAenGluThr 54
|||||

Db 61 CAGGAGCGCGCGTCTCTGAACTGTAGTACAGACACTGCTGCTGAGATGAACA 120
|||||

QY 55 ValGluValIleSerGluMetPheAspLeuGlnProThrCysLeuGlnThrArgLeu 74
|||||

Db 121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCTG 180
|||||

QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
|||||

Db 181 GAGTGTACAAAGCAGGCGCTGCGGGGCGAGCCTCACCAGCTCAAGGGCCCTTGACCATG 240
|||||

QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
|||||

Db 241 ATGGCCAGGCACTTACAAAGCAGCAGCTGCCCTCCAAACCCGCGAACTTCTGTTGCAACCCAG 300
|||||

QY 115 IleIleThrPheGluSerPheLysGluAenLeuLysAspPheLeuLeuValIleProPhe 134
|||||

Db 301 ATTATCACCTTTGAAGATTTCAGAGAACCTCGAGACTTCTGCTGTGTCATCCCTTT 360
|||||

QY 135 AspCysTrpGluProValGlnGlu 142
|||||

Db 361 GACTGCTGGGAGCCAGTCCAGGAG 384
|||||

RESULT 8

US-08-446-872A-176

; Sequence 176, Application US/08446872A

; Patent No. 6361977

; GENERAL INFORMATION:

; APPLICANT: Abrams, Mark A.

; APPLICANT: Bauer, S. C.

; APPLICANT: Braford-Goldberg, Sarah R.

; APPLICANT: Caparon, Mairé H.

; APPLICANT: Easton, Alan M.

; APPLICANT: Klein, Barbara K.

; APPLICANT: McKearn, John P.

; APPLICANT: Olin, Peter O.

; APPLICANT: Paik, Kumnan

; APPLICANT: Thomas, John W.

; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis

; TITLE OF INVENTION: Fusion Protein

; NUMBER OF SEQUENCES: 197

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,

; ADDRESSEE: Corporate Patent Dept.

; STREET: P. O. Box 5110

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60680

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,872A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/192,325

; FILING DATE: 14-FEB-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bennett, Dennis A.

; REGISTRATION NUMBER: 34,547

; REFERENCE/DOCKET NUMBER: C-2790/1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314)737-6986

; TELEFAX: (314)737-6972

; INFORMATION FOR SEQ ID NO: 176:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-446-872A-176

Alignment Scores:
Pred. No.: 2,23e-76 Length: 402
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x US-08-446-872A-176 (1-402)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
DB 1 ATGGCACCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 60
QY 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 61 CAGGAGCGCGGCTCTCTGTAACCTGAGTAGAGACTGCTGCTGAGATGAATGAACA 120
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 121 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGGACTTGCCCTACAGACCCGCTG 180
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 181 GAGCTGTACAGAGCGGCTGCGGGCAGGCTCACCAGCTCAAGGGCCCCCTTGACCATG 240
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 241 ATGGCCAGCCACTACAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTCTGTGCAACCCAG 300
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
DB 301 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAGGACTTCCCTGCTTGTCTATCCCTTT 360
QY 135 AspCysTrpGluProValGlnGlu 142
DB 361 GACTGCTGGAGCCAGTCCAGGAG 384

RESULT 9

US-08-762-227A-176
Sequence 176, Application US/08762227A
Patent No. 6436387

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Ollins, Peter O.
Paik, Kumnan
Thomas, John W.

TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion Protein

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60680

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/762,227A
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 470-6501

TELEFAX: (708) 470-6881

INFORMATION FOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

LENGTH: 402 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 176:

US-08-762-227A-176

Alignment Scores:
Pred. No.: 2,23e-76 Length: 402
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x US-08-762-227A-176 (1-402)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
DB 1 ATGGCACCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 60
QY 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 61 CAGGAGCGCGGCTCTCTGTAACCTGAGTAGAGACTGCTGCTGAGATGAATGAACA 120
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 121 GTAGAAGTGATATCAGAAATGTTGACCTCCAGGAGCGGACTTGCCCTACAGACCCGCTG 180
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 181 GAGCTGTACAGAGCGGCTGCGGGCAGGCTCACCAGCTCAAGGGCCCCCTTGACCATG 240
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 241 ATGGCCAGCCACTACAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTCTGTGCAACCCAG 300
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
DB 301 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAGGACTTCCCTGCTTGTCTATCCCTTT 360
QY 135 AspCysTrpGluProValGlnGlu 142
DB 361 GACTGCTGGAGCCAGTCCAGGAG 384

RESULT 10

PCT-US95-01185-176

Sequence 176, Application PC/TUS9501185

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion

TITLE OF INVENTION: Protein

NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 02-FEB-1995
APPLICATION NUMBER: PCT/US95/01185

PRIOR APPLICATION DATA:
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/192325

INFORMATION FOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

LENGTH: 402 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-01185-176

Alignment Scores:
Pred. No.: 2,236-76 Length: 402
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 5 Gaps: 0

US-10-723-083-2 (1-142) x PCT-US95-01185-176 (1-402)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
DB 1 ATGGCACCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 60
QY 35 GlnGluAlaArgArgLeuLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 61 CAGGAGCGCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 120
QY 55 ValGluValIleSerGluMetPheAspLeuGlnProTrpCysLeuGlnThrArgLeu 74
DB 121 GTAGAAGTGATATCAGAAATGTTGACCTCCAGAGCCGACTTGCCTCAGACCCGCTG 180
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 181 GAGCTGTACAGCAGGCGCTGCGGGCAGCCTCACCAGCTCAAGGCGCCCTTGACCATG 240
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 241 ATGGCCAGGCACCTACCAAGCAGCAGCTGCCCTCCAAACCCGGAACCTTCTGTGCAACCCAG 300
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
DB 301 ATTATCACCTTTGAAAGTTTCAAGAGAACCTTCAAGGACTTCTGCTGTGTCATCCCTTT 360
QY 135 AspCysTrpGluProValGlnGlu 142
DB 361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 11

US-08-469-318-69

Sequence 69, Application US/08469318

Patent No. 6022535

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion

NUMBER OF SEQUENCES: 196

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/446,872

FILING DATE:

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 822 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-469-318-69

Alignment Scores:

Pred. No.: 6,66-76 Length: 822

Score: 678.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 88.63% Indels: 0

DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x US-08-469-318-69 (1-822)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
DB 439 ATGGCACCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 498
QY 35 GlnGluAlaArgArgLeuLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 499 CAGGAGCGCGGCTGTTCCCGTCTACCCAGCGGTGGGAACACGTAATGCCATC 558
QY 55 ValGluValIleSerGluMetPheAspLeuGlnProTrpCysLeuGlnThrArgLeu 74
DB 559 GTAGAAGTGATATCAGAAATGTTGACCTCCAGAGCCGACTTGCCTCAGACCCGCTG 618
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 619 GAGCTGTACAGCAGGCGCTGCGGGCAGCCTCACCAGCTCAAGGCGCCCTTGACCATG 678
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 679 ATGGCCAGGCACCTACCAAGCAGCAGCTGCCCTCCAAACCCGGAACCTTCTGTGCAACCCAG 738
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
DB 739 ATTATCACCTTTGAAAGTTTCAAGAGAACCTTCAAGGACTTCTGCTGTGTCATCCCTTT 798
QY 135 AspCysTrpGluProValGlnGlu 142
DB 799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 12

US-08-468-609A-69

Sequence 69, Application US/08468609A

Patent No. 6030812

GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.

APPLICANT: Bauer, S. C.

APPLICANT: Braford-Goldberg, Sarah R.

APPLICANT: Caparon, Maïre H.

APPLICANT: Easton, Alan M.

APPLICANT: Klein, Barbara K.

APPLICANT: McKearn, John P.

APPLICANT: Oline, Peter O.

APPLICANT: Paik, Kumnan

APPLICANT: Thomas, John W.

TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-609A-69

Alignment Scores:
Pred. No.: 6.6e-76 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x US-08-468-609A-69 (1-822)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
DB 439 ATGGCAGCGGCTGTTCCCGTCCCGCTTACCCAGCGCGTGGAAACACGTGATGCCATC 498
QY 35 GlnGluAlaArgArgLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 499 CAGGAGCGCGGCTCTCTGAACCTGAGTAGAGACACTGCTGAGATGAATGAACA 558
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
DB 559 GTAGAAGTATATACAGAAATGTTTACCTCCAGAGCCGACTTGCCTCAGACCCGCGTG 618
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
DB 619 GAGCTGTACAAGCAGGCGCTCGCGGCGACCTCACCAGCTCAAGGCGCCCTTGACCATG 678
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
DB 679 ATGGCCAGGCACCTACAAAGCAGCAGCTCCCTCCAAACCCCGGAACTTCTGTGCAACCCAG 738
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
DB 739 ATTATCACCTTTGAAGATTTCAAAGAACCTGAGGACTTCTGCTGTGTCATCCCTTT 798
QY 135 AspCysTrpGluProValGlnGlu 142
DB 799 GACTGTGGAGGCGAGTCCAGGAG 822

RESULT 13
US-08-446-872A-69
Sequence 69, Application US/08446872A
Patent No. 6361977
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Caparon, Mair H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olins, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-446-872A-69

Alignment Scores:
Pred. No.: 6.6e-76 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 3 Gaps: 0

US-10-723-083-2 (1-142) x US-08-446-872A-69 (1-822)

QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
DB 439 ATGGCAGCGGCTGTTCCCGTCCCGCTTACCCAGCGCGTGGAAACACGTGATGCCATC 498
QY 35 GlnGluAlaArgArgLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
DB 499 CAGGAGCGCGGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACA 558
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74

Db 559 GTAGAAGTGAATCAGAAATGTTTGACCTCCAGAGCCGACTTGCCCTACAGACCCGCCCTG 618
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 619 GAGCTGTACAAGCAGGCGCTGCGGGCAGCCTCACCAAGCTCAAGGCGCCCTTGACCATG 678
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 679 ATGGCCAGCCACTACCAAGCAGCAGCTCCCTCCAAACCCCGGAAACTTCTCTGTGCAACCCAG 738
QY 115 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
Db 739 ATTATCACCTTGAAGATTTCAAAGAGACCTGAGGACTTCTGCTGTGTCATCCCTTT 798
QY 135 AspCysTrpGluProValGlnGlu 142
Db 799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 14
US-08-762-227A-69
; Sequence 69, Application US/08762227A
; Patent No. 6436387
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Bradford-Goldberg, Sarah R.
; Caparon, Mairé H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Ollins, Peter O.
; Paik, Kumnan
; Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762.227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-08-762-227A-69
Alignment Scores:
Pred. No.: 6.6e-76 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 3 Gaps: 0
US-10-723-083-2 (1-142) x US-08-762-227A-69 (1-822)
QY 15 MetAlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
Db 439 ATGGCACCAGGCTGTTCCCGCTACCCAGCCGTGGGAACACGTAATGCCATC 498
QY 35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
Db 499 CAGGAGGCCCGCGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACA 558
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db 559 GTAGAAGTGAATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCCTACAGACCCGCCCTG 618
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 619 GAGCTGTACAAGCAGGCGCTGCGGGCAGCCTCACCAAGCTCAAGGCGCCCTTGACCATG 678
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 679 ATGGCCAGCCACTACCAAGCAGCAGCTCCCTCCAAACCCCGGAAACTTCTCTGTGCAACCCAG 738
QY 115 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPhe 134
Db 739 ATTATCACCTTGAAGATTTCAAAGAGACCTGAGGACTTCTGCTGTGTCATCCCTTT 798
QY 135 AspCysTrpGluProValGlnGlu 142
Db 799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 15
PCT-US95-01185-69
; Sequence 69, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01185
; FILING DATE: 02-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192325
; FILING DATE: 14-FEB-1994
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-01185-69
Alignment Scores:
Pred. No.: 6.6e-76 Length: 822
Score: 678.00 Matches: 128

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 88.63%
DB: 5
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-723-083-2 (1-142) x PCT-US95-01185-69 (1-822)

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DB	439	ATGGCACCGGCTCGTTCCTCCCGCTACCCAGCGGTGGGAACACGTGAATGCCATC	498
QY	35	GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr	54
DB	499	CAGGAGCCCGCGGTCTCTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACA	558
QY	55	ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu	74
DB	559	GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGCGCGACTTGCTACAGACCCGCTG	618
QY	75	GluLeuTyrllysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet	94
DB	619	GAGCTGTACAAGCAGGGCCCTGCGGGCAGCCTCACCAGCTCAAGGGCCCTTGACCATG	678
QY	95	MetAlaSerHisTyrllysGlnHisCysProProThrProGluThrSerCysAlaThrGln	114
DB	679	ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAAACCCGGAACCTTCCTGTGCAACCCAG	738
QY	115	IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe	134
DB	739	ATTATCACCTTTGAAGTTTCAAGAGAACCTGAGGACTTCCTGCTGTGTCATCCCTTT	798
QY	135	AspCysTrpGluProValGlnGlu	142
DB	799	GACTGCTGGGAGCCAGTCCAGGAG	822

Search completed: March 11, 2005, 20:27:22
Job time : 167 secs

GenCore version 5.1.6
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Run on: March 11, 2005, 19:37:32 ; Search time 505 Seconds
(without alignments)
1672.655 Million cell updates/sec

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Perfect score: 765
Sequence: 1 MHHHHHSGIGRMAPARS.....ENKDLFLVLPDCEPVOE 142

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Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	765	100.0	429	19	US-10-723-083-3	Sequence 3, Appli
2	765	100.0	458	19	US-10-723-083-1	Sequence 1, Appli
3	682	89.2	777	16	US-10-083-446-55	Sequence 55, Appl
4	678	88.6	402	16	US-10-083-446-176	Sequence 176, App
5	678	88.6	822	16	US-10-083-446-69	Sequence 69, Appl
6	678	88.6	903	16	US-10-083-446-66	Sequence 66, Appl
7	675	88.2	2211	17	US-10-609-346-9	Sequence 9, Appli
8	673	88.0	429	17	US-10-449-831A-141	Sequence 141, App
9	673	88.0	435	9	US-09-826-025-8	Sequence 8, Appli
10	673	88.0	435	14	US-10-083-590-14	Sequence 14, Appl
11	673	88.0	435	17	US-10-188-056-31	Sequence 31, Appl
12	673	88.0	435	17	US-10-188-056-32	Sequence 32, Appl
13	673	88.0	435	17	US-10-411-037-17	Sequence 17, Appl
14	673	88.0	435	17	US-10-411-026-17	Sequence 17, Appl
15	673	88.0	435	17	US-10-410-962-17	Sequence 17, Appl
16	673	88.0	435	17	US-10-411-049-17	Sequence 17, Appl
17	673	88.0	435	18	US-10-410-930-17	Sequence 17, Appl
18	673	88.0	435	18	US-10-410-997-17	Sequence 17, Appl
19	673	88.0	435	18	US-10-411-012-17	Sequence 17, Appl
20	673	88.0	435	18	US-10-287-994-17	Sequence 17, Appl
21	673	88.0	435	18	US-10-410-913-17	Sequence 17, Appl
22	673	88.0	435	18	US-10-785-577-8	Sequence 8, Appli
23	673	88.0	435	19	US-10-410-980-17	Sequence 17, Appl
24	673	88.0	448	17	US-10-609-346-19	Sequence 19, Appl
25	673	88.0	505	18	US-10-688-845-82	Sequence 82, Appl
26	673	88.0	579	17	US-10-449-831A-187	Sequence 187, App
27	673	88.0	781	17	US-10-447-315-20	Sequence 20, Appl
28	673	88.0	789	16	US-10-131-985-16	Sequence 16, Appl
29	673	88.0	789	19	US-10-901-417-16	Sequence 16, Appl
30	673	88.0	1011	13	US-10-044-090-509	Sequence 509, App
31	673	88.0	1318	14	US-10-228-811-3	Sequence 3, Appli
32	673	88.0	1833	9	US-09-783-708-2	Sequence 7, Appli
33	673	88.0	2070	9	US-09-821-883-7	Sequence 4, Appli
34	669	87.5	767	18	US-10-666-122-4	Sequence 6, Appli
35	669	87.5	767	18	US-10-666-122-6	Sequence 30, Appl
36	669	87.5	767	19	US-10-278-698-30	Sequence 544, App
37	669	87.5	767	19	US-10-278-698-544	Sequence 19, Appl
38	668	87.3	381	9	US-09-821-883-19	Sequence 33, Appl
39	668	87.3	435	17	US-10-188-056-33	Sequence 34, Appl
40	668	87.3	435	17	US-10-188-056-34	Sequence 191, App
41	668	87.3	496	16	US-10-267-384-191	Sequence 19, Appl
42	668	87.3	737	15	US-10-081-969-19	Sequence 21, Appl
43	668	87.3	756	15	US-10-177-390-21	Sequence 180, App
44	668	87.3	756	17	US-10-351-157-180	Sequence 165, App
45	668	87.3	756	17	US-10-352-554-165	

ALIGNMENTS

RESULT 1
US-10-723-083-3
; Sequence 3, Application US/10723083
; Publication No. US20050050602A1
; GENERAL INFORMATION:
; APPLICANT: Altosaar, Ilimar
; APPLICANT: Sardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Ganz, Peter
; APPLICANT: Tackaberry, Eillean
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: 08-898901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 429

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(429)
OTHER INFORMATION:
US-10-723-083-3

Alignment Scores:
Pred. No.: 2,88e-92 Length: 429
Score: 765.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-10-723-083-2 (1-142) x US-10-723-083-3 (1-429)

QY 1 MetHisHisHisHisHisSerSerGlyIleGluGlyArgMetAlaProAlaArgSer 20
Db 1 ATGCACACACACACACACCTCTCCGGCATCGAGGGCCGCATGCCACCCCGCGGTCA 60
QY 21 ProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeu 40
Db 61 CCAGCCCCAGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGCGGTCTC 120
QY 41 LeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGlu 60
Db 121 CTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTAGATATCAGAA 180
QY 61 MetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrlsGlnGly 80
Db 181 ATGTTTGACCTCCAGGAGCGCATCTGCCTACAGACCCGCTGGAGCTGTACAGCAGGCG 240
QY 81 LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrls 100
Db 241 CTGCGGGGAGCCTCAACAGCTCAAGGGCCCTTGACCATGATGATGCCAGCCACTACAAG 300
QY 101 GlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIleThrPheGluSer 120
Db 301 CAGCATGCGCTCCACCCCGGAACTTCTGTGCAACCCAGATTATCATCCTTTGAAAGT 360
QY 121 PheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAspCysTrpGluProVal 140
Db 361 TTCAAGAGAACCTGAAGGACTTCTGCTGTTCATCCCTTTGACTGCTGGAGCCAGTC 420
QY 141 GlnGlu 142
Db 421 CAGGAG 426

RESULT 2

US-10-723-083-1
Sequence 1, Application US/10723083
Publication No. US20050050602A1
GENERAL INFORMATION:
APPLICANT: Altosar, Illimar
APPLICANT: Sardan, Ravinder
APPLICANT: Dudani, Aail
APPLICANT: Ganz, Peter
APPLICANT: Tackaberry, Eileen
TITLE OF INVENTION: Production of GM-CSF in Plants
FILE REFERENCE: 08-89801US
CURRENT APPLICATION NUMBER: US/10/723,083
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: Canada 2,410,702
PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: CDS
LOCATION: (10)..(438)
OTHER INFORMATION:
US-10-723-083-1

Alignment Scores:
Pred. No.: 3,15e-92 Length: 458
Score: 765.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-10-723-083-2 (1-142) x US-10-723-083-1 (1-458)

QY 1 MetHisHisHisHisHisSerSerGlyIleGluGlyArgMetAlaProAlaArgSer 20
Db 10 ATGCACACACACACACCTCTCCGGCATCGAGGGCCGCATGCCACCCCGCGCAGC 69
QY 21 ProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeu 40
Db 70 CCGAGCCCCCTCCACCGCGCTGGGAGCACGTGAACCGCATCCAGGAGGCCCGCAGGCTC 129
QY 41 LeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGlu 60
Db 130 CTCAACCTCTCCCGCGACACCGCCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAG 189
QY 61 MetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrlsGlnGly 80
Db 190 ATGTTTGATCTCCAGGAGCGCATCTGCCTCCAGACCCGCTCGAGCTGTACAGCAGGCG 249
QY 81 LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrls 100
Db 250 CTCCCGGGCAGCTCACCAGCTCAAGGGCCGCTCACCATGATGGCTCCCATACAG 309
QY 101 GlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIleThrPheGluSer 120
Db 310 CAGCATGCGCTCCACCCCGGAGACCTCTCGCGCACCCAGATCATCACCTTCGAGAGC 369
QY 121 PheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAspCysTrpGluProVal 140
Db 370 TTCAAGGAGAACCTCAAGGACTTCTCTCTCGTATCCCGTTTCGACTGCTGGAGCGGTTG 429
QY 141 GlnGlu 142
Db 430 CAGGAG 435

RESULT 3

US-10-083-446-55
Sequence 55, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:

APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Mair H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/083,446
  FILING DATE: 26-Feb-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/762,227
  FILING DATE: 09-DEC-1996
  APPLICATION NUMBER: US 08/192,325
  FILING DATE: 14-FEB-1994
  APPLICATION NUMBER: US 08/446,872
  FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: S. Christopher Bauer
  REGISTRATION NUMBER: 42,305
  REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (636)737-6257
  TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 55:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 777 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-083-446-55

```

Alignment Scores:		
Pred. No.:	8,048-81	Length:
Score:	682.00	Matches:
Percent Similarity:	97.01%	Conservative:
Best Local Similarity:	97.01%	Mismatches:
Query Match:	89.15%	Indels:
DB:	16	Gaps:
	16	
		777
		130
		0
		4
		0
		0
		0

US-10-723-083-2 (1-142) x US-10-083-446-55 (1-777)

QY	9	SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerThrGlnProTrp	28
DB	376	TCTGGCGGCGGCTCCAACATGCGCTCGTTCCCGCTCCCGCTACCCAGCGGTGG	435
QY	29	GluHisValAsnAlaIleGlnGluAlaArgGluLeuAsnLeuSerArgAspThrAla	48
DB	436	GAACACGTTGAATGCCATCCAGAGGCCGGCGGTCTCTGAACCTGAGTAGAGACACTGTCT	495
QY	49	AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr	68
DB	496	GCTGAGATGATGAACAAGTAGTAGTATATCAGAAATGTTGACCTTCAGAGGCCGACT	555
QY	69	CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu	88
DB	556	TGCCTACAGACCCGCGCTGGAGCTGTACAAGCAGGGCCCTGCGGGGCAGCCCTCACCAAGCTC	615
QY	89	LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu	108
DB	616	AAGGGGCCCTTGACCATGATGCGCAGGCACCTACAAAGCAGCACCTGCCCTCCAAACCCCGGAA	675
QY	109	ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe	128
DB	676	ACTTCTGTGCACCCACGATTATCACCTTTGAAAGTTTCAAGAGAACCTTGAAGGACTTC	735
QY	129	LeuLeuValIleProPheAspCysTrpGluProValGlnGlu	142
DB	736	CTGCTTGTCATCCCTTTTGACTGCTGGGAGCGCACTTCAGGAG	777

RESULT 4
US-10-083-446-176

```

; Sequence 176, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
;      Bauer, S. C.
;      Braford-Goldberg, Sarah R.
;      Caparon, Mairé H.
;      Easton, Alan M.
;      Klein, Barbara K.
;      McKearn, John P.
;      Ollins, Peter O.
;      Paik, Kuman
;      Thomas, John W.
;
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;      Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSES: S. Christopher Bauer, Pharmacia Corporation
;      Corporate Patent Dept., Mail Zone 04E
;
;      STREET: 800 N. Lindbergh
;      CITY: St. Louis
;      STATE: Missouri
;      COUNTRY: USA
;      ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,446
; FILING DATE: 26-Feb-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/762,227
; FILING DATE: 09-DEC-1996
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 08/446,872
; FILING DATE: 06-JUN-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: S. Christopher Bauer
; REGISTRATION NUMBER: 42,305
; REFERENCE/DOCKET NUMBER: C-2790/6
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (636)737-6257
; TELEFAX: (636)737-5452
;
; INFORMATION FOR SEQ ID NO: 176:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 176:
;
; US-10-083-446-176
;
; Alignment Scores:
; Pred. No.: 1,1e-80 Length: 402
; Score: 678.00 Matches: 128
; Percent Similarity: 100.00% Conservatives: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 88.63% Indels: 0
; DB: 16 Gaps: 0

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Qy 15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
Db 1 ATGGACACCGGCTCGTTCCCGCTCCCGCTACCCAGCCGTGGGAACACGTCGAATGCCATC 60
Qy 35 GlnGluAlaArgArgGluLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54

Db 61 CAGGAGGCCGGCGTCTCTGAACCTGAGTAGACACACTGCTGCTGAGATGAATGAACA 120
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db 121 GTAGAGTGATATCAGAAATGTTTGACCTCAGAGCGGACTTGCCCTACAGACCCGGCTG 180
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 181 GAGCTGTACAAGCAGGCGCTGCGGGGAGCCTCACCAGCTCAAGGGCCCTTGACCATG 240
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 241 ATGCCAGCAGCACTACAAGCAGCACTGCCCTCCAAACCCGGAAACTTCTCTGCAACCCAG 300
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
Db 301 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGAGGACTTCTGCTTGTTCATCCCTTT 360
QY 135 AspCysTrpGluProValGlnGlu 142
Db 361 GACTGCTGGGAGCAGTCCAGGAG 384

RESULT 5

US-10-083-446-69

; Sequence 69, Application US/10083446

; Publication No. US20030185790A1

; GENERAL INFORMATION:

; APPLICANT: Abrams, Mark A.

; Bauer, S. C.

; Braford-Goldberg, Sarah R.

; Caparon, Mairé H.

; Easton, Alan M.

; Klein, Barbara K.

; McKearn, John P.

; Olin, Peter O.

; Paik, Kuman

; Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation

STREET: 800 N. Lindbergh

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6

TELEPHONE: (636)737-6257

TELEFAX: (636)737-5452

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

; LENGTH: 822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-083-446-69

Alignment Scores:

Pred. No.: 2,986-80 Length: 822
Score: 678.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 16 Gaps: 0

US-10-723-083-2 (1-142) x US-10-083-446-69 (1-822)

QY 15 MetAlaProAlaArgSerProSerProThrGlnProThrGluHisValAsnAlaIle 34
Db 439 ATGGCACCGGCTCGTTCCCGTCTACCCAGCCGTGGGACACAGTGAATGCCATC 498
QY 35 GlnGluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMethenGluThr 54
Db 499 CAGGAGGCCCGCGTCTCTCTGAACCTGAGTAGACACACTGCTGCTGAGATGAACA 558
QY 55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
Db 559 GTAGAAGTGATATCAGAAATGTTTACCTCCAGGAGCCGACTTGCTTACAGACCCGCTG 618
QY 75 GluLeuTyrlsGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
Db 619 GAGCTGTACAAGCAGGCGCTGCGGGGAGCCTCACCAGCTCAAGGGCCCTTGACCATG 678
QY 95 MetAlaSerHisTyrlsGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
Db 679 ATGGCAGCAGCACTACAAGCAGCAGTCCCTCCCAACCCCGGAAACTTCTGTGCAACCCAG 738
QY 115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
Db 739 ATTATCACCTTTGAAAGTTTCAAGAGAACCTGGAAGGACTTCTCTGCTTGTATCCCTTT 798
QY 135 AspCysTrpGluProValGlnGlu 142
Db 799 GACTGCTGGGAGCAGTCCAGGAG 822

RESULT 6

US-10-083-446-66

; Sequence 66, Application US/10083446

; Publication No. US20030185790A1

; GENERAL INFORMATION:

; APPLICANT: Abrams, Mark A.

; Bauer, S. C.

; Braford-Goldberg, Sarah R.

; Caparon, Mairé H.

; Easton, Alan M.

; Klein, Barbara K.

; McKearn, John P.

; Olin, Peter O.

; Paik, Kuman

; Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation

STREET: 800 N. Lindbergh

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63167

COMPUTER READABLE FORM:


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; SEQ ID NO 141
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
; US-10-449-831A-141

Alignment Scores:
Pred. No.: 5,58e-80 Length: 429
Score: 673.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.97% Indels: 0
DB: 17 Gaps: 0

US-10-723-083-2 (1-142) x US-10-449-831A-141 (1-429)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProThrGluHisValAsnAlaIleGln 35
Db 49 GCACCGCGCGCTCGCCAGCCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAG 108
QY 36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
Db 109 GAGGCGCGCGCTCTCTGAACTGAGTAGACACTGCTGCTGAGATGAATGAAACAGTA 168
QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
Db 169 GAAGTCATCTCAGAAATGTTGACCTCCAGGAGCCGACCTGCTCAGACCCGCTGGAG 228
QY 76 LeuTyLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
Db 229 CTGTACAAGCAGGCGCTCGGGGCGGCTCACCAGCTCAAGGGCCCTTGACCATGATG 288
QY 96 AlaSerHisTyLysGlnHisCysProThrProThrGluThrSerCysAlaThrGlnIle 115
Db 289 GCAGGCACCTACAAGCAGCAGCTGCTCCCAACCCCGGAAACTTCTGTGTCACACCCAGAT 348
QY 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
Db 349 ATCACCTTTGAAGATTTCAAAGAGAACCTGAGGACTTTCTGCTTGTCTATCCCTTTGAC 408
QY 136 CysTrpGluProValGlnGlu 142
Db 409 TGCTGGAGCCAGTCCAGGAG 429

RESULT 9
US-09-826-025-8
; Sequence 8, Application US/09826025
; Patent No. US20020162123A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Combination Immunogene Therapy
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/826,025
; FILING DATE: 04-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/838,702
```

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; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CHANG-02687
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-826-025-8

Alignment Scores:
Pred. No.: 5,69e-80 Length: 435
Score: 673.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.97% Indels: 0
DB: 9 Gaps: 0

US-10-723-083-2 (1-142) x US-09-826-025-8 (1-435)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProThrGluHisValAsnAlaIleGln 35
Db 52 GCACCGCGCGCTCGCCAGCCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111
QY 36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
Db 112 GAGGCGCGCGCTCTCTGAACTGAGTAGACACTGCTGCTGAGATGAATGAAACAGTA 171
QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
Db 172 GAAGTCATCTCAGAAATGTTGACCTCCAGGAGCCGACCTGCTCAGACCCGCTGGAG 231
QY 76 LeuTyLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
Db 232 CTGTACAAGCAGGCGCTCGGGGCGGCTCACCAGCTCAAGGGCCCTTGACCATGATG 291
QY 96 AlaSerHisTyLysGlnHisCysProThrProThrGluThrSerCysAlaThrGlnIle 115
Db 292 GCCAGCCACTACAGCAGCAGCTGCCCTCAACCCCGGAAACTTCTGTGTCACACCCAGAT 351
QY 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
Db 352 ATCACCTTTGAAGATTTCAAAGAGAACCTGAGGACTTTCTGCTTGTCTATCCCTTTGAC 411
QY 136 CysTrpGluProValGlnGlu 142
Db 412 TGCTGGAGCCAGTCCAGGAG 432

RESULT 10
US-10-083-590-14
; Sequence 14, Application US/10083590
; Publication No. US20030027257A1
; GENERAL INFORMATION:
; APPLICANT: IATROU, Kostas
; APPLICANT: FARRELL, Patrick J.
; APPLICANT: BEHIE, Leo A.
; TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF
; FILE REFERENCE: 028722-207
; CURRENT APPLICATION NUMBER: US/10/083,590
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/256,694
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24
; APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136,421
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Human
US-10-083-590-14

Alignment Scores:
Pred. No.: 5,698-80 Length: 435
Score: 673.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.97% Indels: 0
DB: 14 Gaps: 0

US-10-723-083-2 (1-142) x US-10-083-590-14 (1-435)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProTTPGluHisValAlaAlaGln 35
DB 52 GCACCGCGCGCTCGCCAGCCCGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111
QY 36 GluAlaArgLeuLeuLeuLeuSerArgAspThrAlaAlaGluMetAenGluThrVal 55
DB 112 GAGGCCGCGCTCTCTGAACCTGTAGTAGACACTGCTGCTGAGATGAATGAACAGTA 171
QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
DB 172 GAAGTCATCTCAGAAATGTTGACCTCCAGGAGCCAGCTGACCAAGCTCAAGCGCCCTGGAG 231
QY 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
DB 232 CTGTACAGCAGGCGCTCGCGGCGCAGCTCACCAGCTCAAGCGCCCTTGACCATGATG 291
QY 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
DB 292 GCAGGCCACTACAAGCAGCACTGCCCTCCAAACCCCGGAAACTTCTGTGTGAACCCAGATT 351
QY 116 IleThrPheGluSerPheLysGluAenLeuLysAspPheLeuValIleProPheAsp 135
DB 352 ATCACCTTTGAAGATTTCAGAGAGAACCTGAAGGACTTTCTGCTGTGATCCCTTTGAC 411
QY 136 CysTTPGluProValGlnGlu 142
DB 412 TGCTGGAGCCAGTCCAGGAG 432

RESULT 11

US-10-188-056-31
; Sequence 31, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188, 056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-31

Alignment Scores:
Pred. No.: 5,698-80 Length: 435
Score: 673.00 Matches: 127

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.97% Indels: 0
DB: 17 Gaps: 0

US-10-723-083-2 (1-142) x US-10-188-056-31 (1-435)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProTTPGluHisValAlaAlaGln 35
DB 52 GCTCCCGCCAGAACGCCAGCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAG 111
QY 36 GluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAenGluThrVal 55
DB 112 GAGGCCAGACGGCTGCTGAACCTGTCCAGAGACACCGCCCGGAGATGAACGAGACCGTG 171
QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
DB 172 GAGGTGATCAGCGAGATGTTCCGACCTGCAGGAGCCACCTGCTGTCGAGACCCGGCTGGAG 231
QY 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
DB 232 CTGTACAGCAGGAGCTCGCGGCGCAGCTGACCAAGCTGAAGGAGCCCTTGACCATGATG 291
QY 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
DB 292 GCAGGCCACTACAAGCAGCACTGCCCTCCACACCCGAGACCGCTGCGCCACCCAGATC 351
QY 116 IleThrPheGluSerPheLysGluAenLeuLysAspPheLeuValIleProPheAsp 135
DB 352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCTGCTGTGATCCCTTCGAC 411
QY 136 CysTTPGluProValGlnGlu 142
DB 412 TGCTGGAGCCGCTGCAGGAG 432

RESULT 12

US-10-188-056-32
; Sequence 32, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188, 056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-32

Alignment Scores:
Pred. No.: 5,698-80 Length: 435
Score: 673.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.97% Indels: 0
DB: 17 Gaps: 0

US-10-723-083-2 (1-142) x US-10-188-056-32 (1-435)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProTTPGluHisValAlaAlaGln 35
DB 52 GCACCGCGCGCTCGCCAGCCCGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111
QY 36 GluAlaArgLeuLeuAenLeuSerArgAspThrAlaAlaGluMetAenGluThrVal 55
DB 112 GAGGCCGCGCGCTCTCTGAACCTGTAGTAGACACTGCTGCTGATGAATGAACAGTA 171

Qy	56	GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu	75
Db	172	GAAAGTCATCTCAGAAATGTTTGACCTCCAGAGCCGAGCTGCCTACAGACCGCGCTGGAG	231
Qy	76	LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet	95
Db	232	CTGTACAGCAGAGGCCCTGGGGGCGAGCTCACAGCTCAAGGGCCCCCTTGACCATGATG	291
Qy	96	AlaSerHisTyrLysGlnHisCysProThrProGluThrSerCysAlaThrGlnIle	115
Db	292	GCCAGCGACCTACAAACAGCACTGCCTCCAAACCCGGAAACTTCCTGTGCACACCGAGATT	351
Qy	116	IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp	135
Db	352	ATCACCTTTGAAAGTTTCAAGAGAACCTTGAGGAGCTTTCGTGTGTGCATCCCCCTTTGAC	411
Qy	136	CysTrpGluProValGlnGlu	142
Db	412	TGCTGGGAGCCAGTCCAGAG	432

RESULT 13

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US-10-411-037-17
; Sequence 17, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFreese, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A
; TITLE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-037-17

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Alignment Scores:		
Pred. No.:	5,69e-80	Length:
Score:	673.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	87.9%	Indels:
DB:	17	Gaps:
		435
		127

US-10-723-083-2 (1-142) x US-10-411-037-17 (1-435)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
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Db 52 GCACCCGCCCGTCGCCAGCCCCAGCAGCGCCCTGGAGCATGTGAATGCCATCCAG 111

Qy	36	GluAlaArgArgLeuLeuAsnLeuSerArgAspThrIaIaLeuMetAsnGluThrVal	55
Db	112	GAGGCCCGCGCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTA	171
Qy	56	GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu	75
Db	172	GAAGTCATCTCAGAAATGTTTGACCTCCAGAGCGGACCTGCCTACAGACCCGCTGGAG	231
Qy	76	LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysIleuLysGlyProLeuThrMetMet	95
Db	232	CTGTACAACAGCGGCTCGGGGCGAGCTCACCAAGCTCAAGGGCCCTTGACCAATGATG	291
Qy	96	AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle	115
Db	292	GCCAGCCACTACAAGCAGCACTGCGCTCCAAACCCCGGAAACTTCTCTGTGCAACCCAGATT	351
Qy	116	IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp	135
Db	352	ATCACCTTTGAAGAATTTCAAGAGAACCTGAGGACTTTTCTGCTGTGTCATCCCTTTGAC	411
Qy	136	CysTrpGluProValGlnGlu	142
Db	412	TGCTGGAGCCAGTCCAGGAG	432

RESULT 14

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US-10-411-026-17
; Sequence 17, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING ME
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10-411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-026-17

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Alignment Scores:		
Pred. No.:	5,698-80	Length:
Score:	673.00	Matches:
Percent Similarity:	100.00%	Mismatches:
Best Local Similarity:	100.00%	Indels:
Query Match:	87.97%	Gaps:
DB:	17	
		435
		127

US-10-723-083-2 (1-142) x US-10-411-026-17 (1-435)

QY 16 AlaProAlaArgSerProSerThrGlnProTyrGluHisValAsnAlaIleGln 35
DB 52 GCACCGCCGCGTCTCGCCAGCCAGCAGCAGCCCTGGAGCATGTGAATGCCATCCAG 111
QY 36 GluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
DB 112 GAGGCCGCGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTA 171
QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
DB 172 GAAGTCATCTCAGAAATGTTGACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAG 231
QY 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuGlyProLeuThrMetMet 95
DB 232 CTGTACAAGCAGGCGCTCGCGGCGCAGCTCAACAGCTCAAGGGCCCTTGACCATGATG 291
QY 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
DB 292 GCCAGCATACAGCAGCAGCTGCGCTCCAAACCCCGGAACTTCTGTGCAACCCAGATT 351
QY 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPheAsp 135
DB 352 ATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTTCTGCTTGTCTATCCCTTTGAC 411
QY 136 CysTyrGluProValGlnGlu 142
DB 412 TGCTGGGAGCCAGTCCAGGAG 432

RESULT 15

US-10-410-962-17
; Sequence 17, Application US/10410962
; Publication No. US2004007836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Deftrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-962-17

Alignment Scores:
Pred. No.: 5.69e-80 Length: 435
Score: 673.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.97% Indels: 0

DB: 17 Gaps: 0
US-10-723-083-2 (1-142) x US-10-410-962-17 (1-435)
QY 16 AlaProAlaArgSerProSerThrGlnProTyrGluHisValAsnAlaIleGln 35
DB 52 GCACCGCCGCGTCTCGCCAGCCAGCAGCAGCCCTGGAGCATGTGAATGCCATCCAG 111
QY 36 GluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
DB 112 GAGGCCGCGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTA 171
QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
DB 172 GAAGTCATCTCAGAAATGTTGACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAG 231
QY 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuGlyProLeuThrMetMet 95
DB 232 CTGTACAAGCAGGCGCTCGCGGCGCAGCTCAACAGCTCAAGGGCCCTTGACCATGATG 291
QY 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
DB 292 GCCAGCATACAGCAGCAGCTGCGCTCCAAACCCCGGAACTTCTGTGCAACCCAGATT 351
QY 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPheAsp 135
DB 352 ATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTTCTGCTTGTCTATCCCTTTGAC 411
QY 136 CysTyrGluProValGlnGlu 142
DB 412 TGCTGGGAGCCAGTCCAGGAG 432

Search completed: March 11, 2005, 21:35:24
Job time : 512 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 18:16:26 ; Search time 2822 Seconds
(without alignments)
1915.353 Million cell updates/sec

Title: US-10-723-083-2

Perfect score: 765

Sequence: 1 MHHHHHSSGIEGRMAPARS.....ENLKDFLLVIFDCWEPVQE 142

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-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool-US10723083/runat.08032005.131716.10436/app.query.fasta_1.327
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cgi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10723083 @CGN 1.1 4352 @runat.08032005.131716.10436 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsal.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	673	88.0	588	2	AW207707
2	673	88.0	658	5	EX111836
3	673	88.0	660	2	BE218982
4	673	88.0	666	1	AI912784
5	673	88.0	672	2	BE671554
6	673	88.0	695	2	BE669962
7	673	88.0	895	2	BE873976
8	668	87.3	584	7	CF341802
9	652	85.2	592	7	CF370966

10	647	84.6	565	2	BF938995
11	647	84.6	585	7	CF370833
12	640	83.7	718	6	CD369973
13	614	80.3	701	5	BU633411
14	563	73.6	666	6	CA307828
15	559	73.1	475	1	AA995402
16	534	69.8	661	6	CD368851
17	480.5	62.8	561	6	CB457551
18	480.5	62.8	672	7	CF614774
19	473	61.8	572	4	BM539160
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23	419	54.8	423	2	AW784714
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27	301.5	39.4	647	2	BB533718
28	269.5	35.2	629	2	BB664267
29	268	35.0	269	7	CF370885
30	260	34.0	517	6	CB430980
31	254	33.2	369	5	BX521029
32	254	32.4	483	1	AI180669
33	245	32.0	244	4	BG236058
34	229	29.9	470	1	AI121878
35	214	28.0	697	9	AG112609
36	171	22.4	160	7	CF341980
37	162	21.2	136	7	CF341168
38	157	20.5	892	9	CR059250
39	102	13.3	935	7	CF264246
40	101	13.2	721	8	AZ969504
41	99.5	13.0	131	8	AF179193
42	98	12.8	372	7	TK144209
43	94	12.3	828	7	CK144209
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ALIGNMENTS

RESULT 1

AW207707

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW207707 588 bp mRNA linear EST 02-DEC-1999
UI-H-B12-age-e-09-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2724184 3', mRNA sequence.

AW207707.1 GI:6507203

AW207707

AW207707.1 GI:6507203

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 588)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence

is likely internal to the message. cDNA library preparation: M.B.

Source: Lab clone distribution: NCI-CGAP clone distribution

Information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

POLYA-No. Location/Qualifiers

1..588

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2724184"

/lab_host="DH10B (Life Technologies)"

FEATURES

source


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Qy      56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
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Qy      76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
Db      439 CTGTACAAGCAGGGCTCGCGGCGCAGCTCACCAGCTCAAGGGCCCTTGACCATGATG 380
Qy      96 AlaSerHisTyrLysGlnHisCysProThrProGluThrSerCysAlaThrGlnIle 115
Db      379 GCCAGCCTACAGAGCAGCACTGCCCTCCACCCCGAAACTTCTGTGCAACCCAGATT 320
Qy      116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
Db      319 ATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTTCTGCTGTGTCATCCCTTTGAC 260
Qy      136 CysTrpGluProValGlnGlu 142
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DEFINITION hv47a07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176532 3'
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            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  BE218982
VERSION     BE218982.1 GI:8906300
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 660)
REFERENCE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Sequencing by: Greg Lennon, Ph.D.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 445.
FEATURES    Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3176532"
            /tissue_type="carcinoid"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Lu24"
            /notes="Organ: lung; Vector: pTT73D-Pac (Pharmacia) with a
            modified polylinker; plasmid DNA from the normalized
            library NCI CGAP Lu5 was prepared, and ss circles were
            made in vitro. Following HAP purification, this DNA was
            used as tracer in a subtractive hybridization reaction.
            The driver was PCR-amplified cDNAs from a pool of 5,000
            clones made from the same library (cloneIDs
            1414920-1417991 and 1520904-1522439). Subtraction by Bento
            Soares and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:

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Pred. No.:      6,88e-63      Length:      660
Score:          673.00      Matches:      127
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    87.97%      Indels:      0
DB:             2      Gaps:      0

US-10-723-083-2 (1-142) x BE218982 (1-660)

Qy      16 AlaProAlaArgSerProSerProThrGlnProTrpGluHisValAsnAlaIleGln 35
Db      56 GCACCCGCGCTCGCCAGCCGAGCAGCGAGCCCTGGAGCATGTGAATGCCATCCAG 115
Qy      36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
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Qy      56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
Db      176 GAAGTCATCTCAGAAATGTTTGAACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAG 235
Qy      76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
Db      236 CTGTACAAGCAGGGCTCGCGGCGCAGCTCACCAGCTCAAGGGCCCTTGACCATGATG 295
Qy      96 AlaSerHisTyrLysGlnHisCysProThrProGluThrSerCysAlaThrGlnIle 115
Db      296 GCCAGCCTACAGAGCAGCACTGCCCTCCACCCCGAAACTTCTGTGCAACCCAGATT 355
Qy      116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
Db      356 ATCACCTTTGAAAGTTTCAAGAGAACCTGAAGGACTTTCTGCTGTGTCATCCCTTTGAC 415
Qy      136 CysTrpGluProValGlnGlu 142
Db      416 TGCTGGAGCCAGTCCAGGAG 436

RESULT 4
LOCUS      AI912784
DEFINITION AI912784
            666 bp      mRNA      linear      EST 18-DEC-1999
            similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  AI912784
VERSION     AI912784.1 GI:5632639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 666)
REFERENCE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Sequencing by: Greg Lennon, Ph.D.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert length: 743
            Seq primer: -40UP from Gibco
            High quality sequence stop: 447.
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            /mol_type="mRNA"
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		Db	392 ATCACCTTGAAGAAGTTTTCAAGAGAACCTTGAGGACTTTTCCTGCTGTGTCATCCCCCTTGAC 451 Homo sapiens (human)
		QY	136 CysTrpGluProValGlnGlu 142
		Db	452 TGCTGGGAGGCCAGTCCAGGAG 472 RESULT 7
		BE873976	
		LOCUS	BE873976 895 bp mRNA linear EST 20-OCT-2000
		DEFINITION	601484045F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886571 ',
		VERSION	mRNA sequence. BE873976
		ACCESSION	BE873976.1 GI:10322752
		KEYWORDS	EST.
		SOURCE	Homo sapiens (human) ORGANISM
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		REFERENCE	1 (bases 1 to 895) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
		AUTHORS	Unpublished (1999)
		TITLE	Contact: Robert Strausberg, Ph.D.
		JOURNAL	Email: cgapbs-r@mail.nih.gov
		COMMENT	Tissue Procurement: DCTD/DTP/Gazdar CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9663 row: j column: 12 High quality sequence stop: 711.
		FEATURES	Location/Qualifiers source 1..895 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3886571" /tissue_type="large cell carcinoma, undifferentiated" /lab_host="DH10B (phage-resistant)" /clone_lib="NIM MGC 69"
		ORIGIN	(note)="Organ: lung; Vector: pCMV-SPORT6; Site: 1: Notl." Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
		Alignment Scores:	Pred. No.: 1.03e-62 Length: 895 Score: 673.00 Matches: 127 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 87.97% Indels: 0 DB: Gaps: 2
		US-10-723-083-2 (1-142) x BE873976 (1-895)	
		QY	16 AlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaileGln 35
		Db	50 GCACCGCCCGCTCCTCGCCAGCCCCAGCCGCTGGAGCATGTGAATGCCATCCAG 109
		QY	36 GluAlaArgArgLeuLeuAsnLeuSerArgaspThrAlalaGluMetAsnGluThrVal 55
		Db	110 GAGGCCCGCGCTCTCTGAACCTGAGTAGACACACTGCTGCTGAGATGAATAACAACAGTA 169
		QY	56 GluValIleSerGluWetPheAspleuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
		Db	170 GAAGTCATCTCAGAATGTTTGAATCTCCAGGAGCGACCTGCCTACAGACCCGCTGGAG 229
		FACTOR PRECURSOR (HUMAN); , mRNA sequence.	
		BE669962	
		VERSION	BE669962.1 GI:10030503
		KEYWORDS	EST.
		SOURCE	Homo sapiens (human)
		ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		REFERENCE	1 (bases 1 to 695) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
		AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
		TITLE	Unpublished (1997)
		JOURNAL	Contact: Robert Strausberg, Ph.D.
		COMMENT	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.; Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 456.
		FEATURES	Location/Qualifiers source 1..695 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3283742" /tissue_type="carcinoid" /lab_host="DH10B" /clone_lib="NCI CGAP Lu24" /note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP lu25 was prepared, and ss circles were used in vitro. Following HAP purification, this DNA was made as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (ClonesIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."
		ORIGIN	
		Alignment Scores:	Pred. No.: 7.38e-63 Length: 695 Score: 673.00 Matches: 127 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 87.97% Indels: 0 DB: Gaps: 2
		US-10-723-083-2 (1-142) x BE669962 (1-695)	
		QY	16 AlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaileGln 35
		Db	92 GCACCGCCCGCTCCTCGCCAGCCCCAGCCGCTGGAGCATGTGAATGCCATCCAG 151
		QY	36 GluAlaArgArgLeuLeuAsnLeuSerArgaspThrAlalaGluMetAsnGluThrVal 55
		Db	152 GAGGCCCGCGCTCTCTGAACCTGAGTAGACACACTGCTGCTGAGATGAATAACAACAGTA 211
		QY	56 GluValIleSerGluWetPheAspleuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
		Db	212 GAAGTCATCTCAGAATGTTTGAATCTCCAGGAGCGACCTGCCTACAGACCCGCTGGAG 271
		QY	76 LeuTyrlvsGlnGlyLyuArgglySerLeuthrylsLysLeuLyssGlvProLeuthrMetMet 95
		Db	272 CTGTACACAGCGGCTCGGGGGAGCCCTCACAGCTCAGGGGCCCTTGACCATGATG 331
		QY	96 AlaserHistyllysGlnHisCysprothrPrroGluThrserCysAlathrgInfile 115

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Qy 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
    |||||
Db 230 CTGTACAAAGCAGGCGCTCGGGGAGGCTTACCAGCTCAAGGCGCCCTTGACCATGATG 289
    |||||
Qy 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
    |||||
Db 290 GCCAGCCACTACAAGCAGCACTGCGCTCCAACCCGGAAACTTCTGTGCAACCCAGATT 349
    |||||
Qy 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
    |||||
Db 350 ATCACCTTTGAAGATTTCAAAGAGAACTCAAGGACTTCTGCTGTGTCATCCCTTTGAC 409
    |||||
Qy 136 CysTrpGluProValGlnGlu 142
    |||||
Db 410 TGCTGGGAGCCAGTCCAGGAG 430

RESULT 8
CF341802 584 bp mRNA linear EST 18-AUG-2003
LOCUS TgESTzyj43f02.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
DEFINITION cDNA clone TgESTzyj43f02.y1 5' similar to SW:CSF2 HUMAN P04141
            GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
            sequence.
ACCESSION CF341802
VERSION CF341802.1 GI:33831915
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
REFERENCE 1 (bases 1 to 584)
AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
        Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M.,
        Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
        Ritter,S., Bennett,J., Franklin,C., Tsagarelisvili,R., Ronko,I.,
        Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
        Toxoplasma EST Project
        Unpublished (2001)
        Contact: Clifton, S.
        Toxoplasma EST Project
        Washington University School of Medicine
        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
        Tel: 314 286 1800
        Fax: 314 286 1810
        Email: toxo@watson.wustl.edu
        Contact David Sibley (toxost@borcim.wustl.edu) for further
        information relating to organism, libraries, or clone availability.
        Seq primer: -40UP from Gibco.
        Location/Qualifiers
            1..584
               /organism="Toxoplasma gondii"
               /mol_type="mRNA"
               /db_xref="taxon:5811"
               /clone="TgESTzyj43f02.y1"
               /dev_stage="Tachyzoite"
               /lab_host="ElectroTen Blue cells (Stratagene)"
               /clone_lib="Tg CAST Tachyzoite cDNA Library"
               /notes="Vector: Modified pBluescript (pBS SK+); Site_1:
        BamHI; Site_2: EcoRI; The cDNA library was constructed by
        Keliang Tang, and Robert Cole at Washington University.
        cDNA was synthesized from poly(A)+ mRNA using the
        template-switching PCR method (SMART cDNA Kit, BD
        Biosciences). First strand cDNA was reverse transcribed
        using the CDS III/3' primer and a 5' template switch
        primer (Smart IV primer). The product of the first strand
        synthesis was PCR amplified using the same primer set and
        the fragments were digested with SfiI. The fragments were
        size selected, ligated into a modified pBluescript vector
        (obtained from Michael White, Montana State University)
        containing directional SfiI sites, and electroporated into
        ElectroTen Blue cells. Vector: SfiI sites were added to
        the multiple cloning region of pBluescript SK+ between the

```

BamHI/EcoRI sites. The modified polylinker has the following sequence: 5'GAATTGGCCATTACGGCC(G)n- insert--GGCCCTGGCCCGACGATCC3' where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."

ORIGIN

Alignment Scores: 2.05e-62 Length: 584
 Pred. No.: 668.00 Matches: 126
 Score: 668.00
 Percent Similarity: 99.21% Conservative: 0
 Best Local Similarity: 99.21% Mismatches: 1
 Query Match: 87.32% Indels: 0
 DB: 7 Gaps: 0

US-10-723-083-2 (1-142) x CF341802 (1-584)

```

Qy 16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
    |||||
Db 84 GCACCGCGCGCTCGCCCGAGCCCGCAGCGAGCCCTGGAGCATGTGAATGCCATCCAG 143
    |||||
Qy 36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
    |||||
Db 144 GAGGCGCGCGCTCTCTGAACCTGAGTGAAGACACTGCTGTGCTGAGATGAATGAACAGTA 203
    |||||
Qy 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
    |||||
Db 204 GAAGTCATCTCAGAAATGTTTACCTCCAGGAGCGACCTGCTACAGACCGCGCTGGAG 263
    |||||
Qy 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
    |||||
Db 264 CTGTACAAAGCAGGCGCTCGGGGAGGCTTACCAGCTCAAGGCGCCCTTGACCATGATG 323
    |||||
Qy 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
    |||||
Db 324 GCCAGCCACTACAAGCAGCACTGCGCTCCAACCCGGAAACTTCTGTGCAACCCAGACT 383
    |||||
Qy 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
    |||||
Db 384 ATCACCTTTGAAGATTTCAAAGAGAACTTCAAGAGAACTTCTGCTGTGTCATCCCTTTGAC 443
    |||||
Qy 136 CysTrpGluProValGlnGlu 142
    |||||
Db 444 TGCTGGGAGCCAGTCCAGGAG 464

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RESULT 9

CF370966

LOCUS

DEFINITION

592 bp mRNA linear EST 27-AUG-2003
 TgESTzyj58e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
 cDNA clone TgESTzyj58e12.y1 5' similar to SW:CSF2 HUMAN P04141
 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
 sequence.

ACCESSION CF370966

VERSION CF370966.1 GI:34318212

KEYWORDS EST.

SOURCE Toxoplasma gondii

ORGANISM Toxoplasma gondii

REFERENCE 1 (bases 1 to 592)

AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,

Clifton,S., Pape,D., Martin,J., Wyllie,T., Dante,M., Marra,M.,

Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,

Ritter,S., Bennett,J., Franklin,C., Tsagarelisvili,R., Ronko,I.,

Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.

Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.

Toxoplasma EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810
 Email: toxo@watson.wustl.edu
 Contact David Sibley (toxost@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.
 Seq primer: -40UP from Gibco.

FEATURES

source

1. 592
 /organism="Toxoplasma gondii"
 /mol_type="mRNA"
 /db_xref="taxon:5811"
 /clone="TgESTzyj58612.y1"
 /dev_stage="Tachyzoite"
 /lab_host="Electroten Blue cells (Stratagene)"
 /clone_lib="Tg CAST Tachyzoite cDNA Library"
 /notes="Vector: Modified pluescript (pBS SK+); Site 1:
 BamHI; Site 2: EcoRI; The cDNA library was constructed by
 Keliang Tang, and Robert Cole at Washington University.
 cDNA was synthesized from poly(A)+ mRNA using the
 template-switching PCR method (SMART cDNA Kit, BD
 Biosciences). First strand cDNA was reverse transcribed
 using the CDS III/3' primer and a 5' template switch
 primer (Smart IV primer). The product of the first strand
 synthesis was PCR amplified using the same primer set and
 the fragments were digested with SfiI. The fragments were
 size selected, ligated into a modified pBluescript vector
 (obtained from Michael White, Montana State University)
 containing directional SfiI sites, and electroporated into
 Electroten Blue cells. Vector: SfiI sites were added to
 the multiple cloning region of pBluescript SK+ between the
 BamHI/EcoRI sites. The modified polylinker has the
 following sequence: 5'GAATTCGGCCATTAGGCC(G)n--insert--
 GGCCGCTGGCCACGATCC3' where n=3-4 G nucleotides.
 WARNING: the library contains a small percentage of cDNAs
 derived from the human host cells. Library materials
 provided by David Sibley, Washington University."

ORIGIN

Alignment Scores:
 Pred. No.: 1.16e-60 Length: 592
 Score: 652.00 Matches: 123
 Percent Similarity: 97.64% Conservative: 1
 Best Local Similarity: 96.85% Mismatches: 3
 Query Match: 85.23% Indels: 0
 DB: 7 Gaps: 0

US-10-723-083-2 (1-142) x CF370966 (1-592)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProThrGluHisValAsnAlaIleGln 35
 |||||
 DB 86 GCACCCGCGCGTCTCTCGAACCTGAGTAGACACTGCTGCTGAGATGATATAGTA 205
 |||||
 QY 36 GluAlaArgLeuLeuLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
 |||||
 DB 146 GAGGCGCGCGTCTCTCGAACCTGAGTAGACACTGCTGCTGAGATGATATAGTA 205
 |||||
 QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
 |||||
 DB 206 GAAGTCATCTCAGAAATGTTTACCTCCAGGAGCGACCTGCTACAGACCCGCTGGAG 265
 |||||
 QY 76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 95
 |||||
 DB 266 CTGTACAGAGGCGCTGCGGGGACGCCCCACCAAGCTCAAGGGCCCCCTTGACCATGATG 325
 |||||
 QY 96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
 |||||
 DB 326 GCACGCACTACAAGCAGCACTGCCCTCCACCCCGGAACTCTCTGTGCAACCCAGACT 385
 |||||
 QY 116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheApp 135
 |||||
 DB 386 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGCTATCCCTTTGAC 445
 |||||
 QY 136 CysTrpGluProValGlnGlu 142
 |||||

Db 446 TGCTGGAGCCAGTCCAGGAG 466

RESULT 10

BF938995

LOCUS

DEFINITION

BF938995 565 bp mRNA linear EST 22-JAN-2001
 7r03f11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3706893 3',
 similar to SM_CSE2 HUMAN P04141 GRANULOCYTE-MACROPHAGE
 COLONY-STIMULATING_FACTOR PRECURSOR ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF938995 1 GI:12356315
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 565)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 497.

FEATURES

source

1. 565
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3706893"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu24"
 /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI CGAP-Lus was prepared, and ss circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (cloneIDs
 141420-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 3.83e-60 Length: 565
 Score: 647.00 Matches: 127
 Percent Similarity: 98.45% Conservative: 0
 Best Local Similarity: 98.45% Mismatches: 0
 Query Match: 84.58% Indels: 2
 DB: 2 Gaps: 0

US-10-723-083-2 (1-142) x BF938995 (1-565)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProThrGluHisValAsnAlaIle-G 35
 |||||
 DB 92 GCACCCGCGCGTCTGCGCCAGCCCGCCAGCGAGCGTGGAGCATGTGAATGCCATCAC 151
 |||||
 QY 35 lngluAlaArgLeuLeuLeuSerArgAspThrAlaAlaGluMetAsnGluThrV 55
 |||||
 DB 152 AGAGAGCCCGGGCTCTCTGGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAG 211
 |||||
 QY 55 aGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuG 75
 |||||
 DB 212 TAGAAGTCATCTCAGAAATGTTTACCTCCAGGAGCGGACCTGCTACAGACCCGCTGG 271
 |||||

QY 75 luLeuTyLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetM 95
 Db 272 AGCTGTACAAGCAGGGCTCGGGGCGACCTCACAGCTCAAGGGCCCTTGACCAIGA 331
 QY 95 etAlaSerHisTyLysGlnHisCysProThrProGluThrSerCysAlaThrGlnI 115
 Db 332 TGGCCAGCCACTACAAGCAGCACTGCCCTCAACCCCGGAACTTCTGTGCAACCCAGA 391
 QY 115 lelleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValleProPheA 135
 Db 392 TTATCACCCTTTGAAGATTCAAGAGAACCTGAAGGACTTCTGCTTGTATCCCTTTG 451
 QY 135 spCysTrpGluProValGlnGlu 142
 Db 452 ACTGCTGGAGCCAGTCCAGGAG 474

RESULT 11

CF370833 585 bp mRNA linear EST 27-AUG-2003
 DEFINITION TgESTzyj55e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
 cDNA clone TgESTzyj55e12.y1 5', similar to SW.CSP2 HUMAN P04141
 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
 sequence.

ACCESSION CF370833
 VERSION CF370833.1 GI:34318079
 KEYWORDS EST.

ORGANISM

Toxoplasma gondii
 Toxoplasma gondii
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

REFERENCE

AUTHORS Tang, K., Cole, R., Sibley, S., Fogarty, S., Ajioka, J. A., White, M.,
 Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,
 Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
 Ritter, E., Bennett, J., Franklin, C., Tsagarelis, V. I., Ronko, I.,
 Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.

TITLE

Toxoplasma EST Project

JOURNAL

Comment: Clifton, S.

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@watson.wustl.edu

Contact David Sibley (toxoeast@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.

FEATURES

source

BamHI/EcoRI sites. The modified polylinker has the
 following sequence: 5'GAATTGGCCATTACGGCC(G)n-- insert--
 GCGGCTCGCCCGACGATCC3' where n=3-4 G nucleotides.
 WARNING: the library contains a small percentage of cDNAs
 derived from the human host cells. Library materials
 provided by David Sibley, Washington University."

ORIGIN

Alignment Scores:
 Pred. No.: 4,01e-60 Length: 585
 Score: 647.00 Matches: 123
 Percent Similarity: 96.85% Conservative: 0
 Best Local Similarity: 96.85% Mismatches: 4
 Query Match: 84.58% Indels: 0
 DB: 7 Gaps: 0

US-10-723-083-2 (1-142) x CF370833 (1-585)

QY 16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
 Db 86 GCACCCGCCCTCGCCCGACGCCCGCCAGCGAGCATGTGAATCCCATCCAG 145
 QY 36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
 Db 146 GAGGCCCGCGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATTTAATAGTA 205
 QY 56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
 Db 206 GAAGTCATCTCAGAAATGTTTACCTCCAGGAGCGACCTGCCTACAGACCCCGCTGGAG 265
 QY 76 LeuTyLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
 Db 266 CTGTACAGCAGCGCTCGGGGCGAGCCCGCCAGCTCAAGGGCCCTTGACCATGATG 325
 QY 96 AlaSerHisTyLysGlnHisCysProThrProGluThrSerCysAlaThrGlnIle 115
 Db 326 GCCAGCCACTACAAGCAGCACTGCCCTCAACCCCGGAACTTCTGTGCAACCCAGACT 385
 QY 116 lleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValleProPheAsp 135
 Db 386 ATCACCCTTTGAAGATTCAAGAGAACCTGAAGGACTTCTGCTGTGTCATCCCCCTTTGAC 445
 QY 136 CysTrpGluProValGlnGlu 142
 Db 446 TGCTGGAGCCAGTCCAGGAG 466

RESULT 12

CD369973/c

LOCUS

DEFINITION

UI-H-FT1-bke-o-08-0-UI-s1 NCI CGAP FT1 Homo sapiens cDNA clone

UI-H-FT1-bke-o-08-0-UI 3', mRNA sequence.

CD369973

CD369973

CD369973.1 GI:31154063

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/cgap.html>

The following repetitive elements were found in this cDNA

sequence: 65-134, >(TAAA)n#Simple_repeat

CD369973 718 bp mRNA linear EST 05-AUG-2004
 UI-H-FT1-bke-o-08-0-UI-s1 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-bke-o-08-0-UI 3', mRNA sequence.

CD369973

CD369973

CD369973.1 GI:31154063

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/cgap.html>

The following repetitive elements were found in this cDNA

sequence: 65-134, >(TAAA)n#Simple_repeat

FEATURES		Location/Qualifiers		source	
Seq primer: M13 FORWARD					
POLYA=Yes.					
QY	97	SerHisTyrLysGlnHisCysProThrProGluThrSerCysAlaThrGlnIle	111		
Db	477	AGCCACTACAAGCAGCACTGCCCTCAACCCCGGAACCTTCTGTGCAACCCAGATTATC	418		
QY	117	ThrPheGluSerPheLysGlnAsnLeuLysAspPheLeuLeuValIleProPheAspCys	136		
Db	417	ACCTTTGAAGTTTCAAGAGAACCTGAAGGACTTTCTGCTGTGCATCCCTTTGACTGC	358		
QY	137	TrpGluProValGlnGlu	142		
Db	357	TGGAGCCAGTCCAGGAG	340		
<p>RESULT 13</p> <p>BU633411/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>UI-H-FL1-bgu-1-15-0-UI.s1 NCI CGAP FL1 Homo sapiens CDNA clone</p> <p>UI-H-FL1-bgu-1-15-0-UI 3', mRNA sequence.</p> <p>BU633411</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>REFERENCE</p> <p>1 (bases 1 to 701)</p> <p>AUTHORS</p> <p>NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.</p> <p>TITLE</p> <p>National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index</p> <p>JOURNAL</p> <p>COMMENT</p> <p>Unpublished (1997)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: cgapsb@mail.nih.gov</p> <p>Tissue Procurement: James Martin</p> <p>CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa</p> <p>CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa</p> <p>Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu</p> <p>The following repetitive elements were found in this CDNA sequence: 1-46, >AT rich#Low_complexity 60-129, >(TAA)n#Simple_repeat</p> <p>Seq primer: M13_FORWARD</p> <p>POLYA=Yes.</p>					
<p>FEATURES</p> <p>source</p> <p>1..701</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="UI-H-FL1-bgu-1-15-0-UI"</p> <p>/tissue_type="Cell lines"</p> <p>/dev_stage="Adult"</p> <p>/lab_host="DH10B (Life Technologies)"</p> <p>/clone_lib="NCI CGAP FL1"</p> <p>/note="Organ: Chondrosarcoma; Vector: pTT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FL1 is a normalized CDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.</p> <p>TAG_TISSUE=Human Lung Alveolar Macrophage</p> <p>TAG_LIB=UI-H-FT1</p> <p>TAG_SEQ=GGCCATGCGG"</p>					
ORIGIN					
<p>Alignment Scores:</p> <p>Pred. No.: 3,06e-59 Length: 718</p> <p>Score: 640.00 Matches: 125</p> <p>Percent Similarity: 99.21% Conservative: 0</p> <p>Best Local Similarity: 99.21% Mismatches: 1</p> <p>Query Match: 83.66% Indels: 1</p> <p>DB: 6 Gaps: 0</p>					
US-10-723-083-2 (1-142) x CD369973 (1-718)					
QY	17	ProAlaArgSerProSerProThrGlnProThrGluHisValAsnAlaIleGlnGlu	36		
Db	716	CCGCGCGCTCGCCAGCCAGCAGCGCCCTGGGAGCATGTGAATGCCATCCAGGAG	657		
QY	37	AlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGlu	56		
Db	656	GCCCGCGGCTCTGAACCTGAGTAGACACTGCTGCTGAGATGAATGAACAGTAGAA	597		
QY	57	ValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeu	76		
Db	596	GTCACTCTCAGAAATGTT-CACCTCCAGGAGCCGACCTGCCTACAGCCCGCTGAGCTG	538		
QY	77	TyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAla	96		
Db	537	TACAACAGCGGCTCGGGGAGGCTCTACCAAGCTCAAGGGCCCTTGACCATGATGCGC	478		

Alignment Scores:

Pred. No.: 2,02e-56 Length: 701
 Score: 514.00 Matches: 120
 Percent Similarity: 98.36% Conservatives: 0
 Best Local Similarity: 98.36% Mismatches: 2
 Query Match: 80.26% Indels: 1
 DB: 5 Gaps: 0

US-10-723-083-2 (1-142) x BU633411 (1-701)

QY 21 ProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeu 40
 DB 699 CCCAGCCCCAGCAGCAGCGCTGGAGCATGTGAATCC-ATCCAGAGGCGCGCGCTC 641
 QY 41 LeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGlu 60
 DB 640 CTGAACCTGAGTAGAGACATGCTGCTGAGATGAATGAACAGTAGAAGTCATCTCAGAA 581
 QY 61 MetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrLysGlnGly 80
 DB 580 ATGTTTGACCTCCAGGAGCGGACCTGCTACAGACCGCGCTGAGCTGTACAGAGGCG 521
 QY 81 LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrLys 100
 DB 520 CTGCGGGGCGAGCCTCAACAGCTCAAGGCGCCCTTGACCATGATGCCAGCCACTACAAG 461
 QY 101 GlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIleThrPheGluSer 120
 DB 460 CACAGTGCCCTCAACCCCGGAACCTTCTGTGCAACCCAGATATATACCTTTGAAGT 401
 QY 121 PheLysGluAsnLeuLysAspPheLeuValIleProPheAspCysTrpGluProVal 140
 DB 400 TTCAAGAGAACCTGAAGGACTTCTGCTGTATCCCTTTGACTGCTGGAGCCAGTC 341
 QY 141 GlnGlu 142
 DB 340 CAGGAG 335

RESULT 14

CA307828/c
 LOCUS CA307828 666 bp mRNA linear EST 05-AUG-2004
 DEFINITION UI-H-FTL-bhx-f-10-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
 CA307828
 VERSION UI-H-FTL-bhx-f-10-0-UI 3', mRNA sequence.
 CA307828.1 GI:24470882
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 666)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Cloning Distribution: Dr. M. Bento Soares, University of Iowa
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-50, >AT_richLow_complexity 64-133,
 >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLVA=Yes.

Location/Qualifiers
 1. .666
 /organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES
source

/db_xref="taxon:9606"
 /clone="UI-H-FTL-bhx-f-10-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP FTL"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is GCCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_L1B=UI-H-FTL
 TAG_SEQ=GGCCATGCCG"

ORIGIN

Alignment Scores:
 Pred. No.: 6.88e-51 Length: 666
 Score: 563.00 Matches: 108
 Percent Similarity: 99.08% Conservatives: 0
 Best Local Similarity: 99.08% Mismatches: 1
 Query Match: 73.59% Indels: 0
 DB: 6 Gaps: 0
 US-10-723-083-2 (1-142) x CA307828 (1-666)
 QY 34 IleGlnGluAlaArgArgLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGlu 53
 DB 665 ATCCAGAGGCGCGCGCTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAA 606
 QY 54 ThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArg 73
 DB 605 ACAGTAGAAGTCATCTCAGAAATGTTTACCTCCAGAGAGCCGACCTGCTACAGACCCCG 546
 QY 74 LeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThr 93
 DB 545 TTGGAGCTGTACAAGCGGCGCTGCGGGGCGAGCCTCACCAAGCTCAAGGGCCCTTGACC 486
 QY 94 MetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThr 113
 DB 485 ATGATGGCCAGCCANTACAAGCAGCAGCTCCCTCCACCCCGGAACCTTCTGTGTGAACC 426
 QY 114 GlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIlePro 133
 DB 425 CAGATTATCACCTTTGAAGATTTCAGAGAGAACCTGAGGACTTTCTGCTGTCATCCCC 366
 QY 134 PheAspCysTrpGluProValGlnGlu 142

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Db      365 TTTGACTGCTGGAGCCAGTCCAGGAG 339
|||||
RESULT 15
AA995402
LOCUS   475 bp mRNA linear EST 27-AUG-1998
DEFINITION
or74f05.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1601601 3'
similar to gb:U11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
FACTOR PRECURSOR (HUMAN); mRNA sequence.
ACCESSION
AA995402
VERSION
AA995402.1 GI:3181891
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 475)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 747 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 308.

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FEATURES

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1..475
Location/Qualifiers
1..475
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601601"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu5"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoma, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

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ORIGIN

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Alignment Scores:
Pred. No.: 12e-50 Length: 475
Score: 559.00 Matches: 119
Percent Similarity: 94.49% Conservative: 1
Best Local Similarity: 93.70% Mismatches: 6
Query Match: 73.07% Indels: 3
DB: 1 Gaps: 0

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US-10-723-083-2 (1-142) x AA995402 (1-475)

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QY      16 AlaProAlaArgSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
|||||
Db      55 GCACCCGCCCGCTCGCCAGCCCGCAGCAGCCCTGGAGCATGTGATGC-ATCCAG 113
|||||
QY      36 GluAlaArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
|||||
Db      114 GAGGCCCGCGCTCTCCTGAACCTGAGTAGACACTGCTGAGATGAATGAACAGTA 173
|||||
QY      56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
|||||

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Db      174 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAG 233
QY      76 LeuTyrLysGlnGlyLeuArgGlySer-LeuThrLysLeuLysGlyProLeuThrMetMe 95
|||||
Db      234 CTGTACAAGCAGGGCCCTGCGTGGCAGTCTCTACCAAGCTCAAGGGGCCCTTGACCATGAT 293
|||||
QY      95 tAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnI 115
|||||
Db      294 GGCACGCCACTACAGCAGCAGCTGCCCTCCAAACCCGGAACCTTCCTTTTGC AAC-CAGAT 352
|||||
QY      115 eileThrPheGluSerPheLysGluAsnLeuLysAspPheLeuValIleProPheAs 135
|||||
Db      353 TATCACCTCTTGNAGTTTCAAGAGAACCTGAAGGACTTCTCTGTGTATCACCATTGA 412
|||||
QY      135 pCysTrpGluProValGln 141
|||||
Db      413 CTGCTGGAGCCAGTCAGG 431
|||||

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Job time : 2828 secs

